



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 115241

TO: Karen A Lacourciere
Location: rem/2d15/2c18
Art Unit: 1635
Monday, March 08, 2004

Case Serial Number: 09/848868

From: Alex Waclawiw
Location: Biotech-Chem Library
Rem 1A71
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Search Notes

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 22:57:56 ; Search time 343 Seconds
(without alignments)
222.938 Million cell updates/sec

Title: US-09-848-868-35

Perfect score: 18
Sequence: 1 ccgcgaagcagctctgc 18

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 200 summaries

Database : N_Geneseq_29Jan04:*

- 1: Geneseq1980s:*
- 2: Geneseq1980s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001as:*
- 5: Geneseq2001bs:*
- 6: Geneseq2002s:*
- 7: Geneseq2003as:*
- 8: Geneseq2003bs:*
- 9: Geneseq2003cs:*
- 10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	ID	Description
1	18	100.0	18	AA519106 Human p53
2	18	100.0	36	AA519107 Human p53
3	18	100.0	37	AA526511 WO 990919
4	18	100.0	140	AAV17739 Human bre
5	18	100.0	255	AAQ74245 p53 antic
6	18	100.0	255	AAV17740 Human bre
7	18	100.0	800	AA159673 Human p53
8	18	100.0	1024	AB283767 Tox1colog
9	18	100.0	1070	AA252304 Human p35
10	18	100.0	1303	AA504533 DNA encod
11	18	100.0	1303	AB573327 DNA encod
12	18	100.0	1303	AA549400 Human p53
13	18	100.0	1307	AAAD00088 Human tum
14	18	100.0	1307	ABX15394 Human p53
15	18	100.0	1317	AA132831 Human p53
16	18	100.0	1317	AAV18151 Nucleotid
17	18	100.0	1317	AAV21414 Human p53
18	18	100.0	1317	AAV44695 Human wtl
19	18	100.0	1317	AA584597 Human p53
20	18	100.0	1317	AAAD1279 Human p53
21	18	100.0	1317	AAAD43529 Human p53
22	18	100.0	1760	AAAT79880 DNA encod
23	18	100.0	1760	AA575765 Human p53

C 24	18	100.0	1760	AA54029 Human col
C 25	18	100.0	1760	ABAD0952 Human p53
C 26	18	100.0	2451	AD222450 HLA-B*6 T
C 27	18	100.0	2600	AA565699 DNA encod
C 28	18	100.0	2605	AA567409 DNA encod
C 29	18	100.0	397	AB509379 Human p53
C 30	18	100.0	436	ACH9668 Human leu
C 31	18	100.0	942	ABK42958 Genomic s
C 32	18	100.0	942	ABK42959 Genomic s
C 33	18	100.0	942	ABK42958 Genomic s
C 34	18	100.0	942	ABK42958 Genomic s
C 35	18	100.0	942	ABK42958 Genomic s
C 36	18	100.0	942	ABK42958 Genomic s
C 37	18	100.0	942	ABK42958 Genomic s
C 38	18	100.0	942	ABK42958 Genomic s
C 39	18	100.0	942	ABK42958 Genomic s
C 40	18	100.0	942	ABK42958 Genomic s
C 41	18	100.0	942	ABK42958 Genomic s
C 42	18	100.0	942	ABK42958 Genomic s
C 43	18	100.0	942	ABK42958 Genomic s
C 44	18	100.0	942	ABK42958 Genomic s
C 45	18	100.0	942	ABK42958 Genomic s
C 46	18	100.0	942	ABK42958 Genomic s
C 47	18	100.0	942	ABK42958 Genomic s
C 48	18	100.0	942	ABK42958 Genomic s
C 49	18	100.0	942	ABK42958 Genomic s
C 50	18	100.0	942	ABK42958 Genomic s
C 51	18	100.0	942	ABK42958 Genomic s
C 52	18	100.0	942	ABK42958 Genomic s
C 53	18	100.0	942	ABK42958 Genomic s
C 54	18	100.0	942	ABK42958 Genomic s
C 55	18	100.0	942	ABK42958 Genomic s
C 56	18	100.0	942	ABK42958 Genomic s
C 57	18	100.0	942	ABK42958 Genomic s
C 58	18	100.0	942	ABK42958 Genomic s
C 59	18	100.0	942	ABK42958 Genomic s
C 60	18	100.0	942	ABK42958 Genomic s
C 61	18	100.0	942	ABK42958 Genomic s
C 62	18	100.0	942	ABK42958 Genomic s
C 63	18	100.0	942	ABK42958 Genomic s
C 64	18	100.0	942	ABK42958 Genomic s
C 65	18	100.0	942	ABK42958 Genomic s
C 66	18	100.0	942	ABK42958 Genomic s
C 67	18	100.0	942	ABK42958 Genomic s
C 68	18	100.0	942	ABK42958 Genomic s
C 69	18	100.0	942	ABK42958 Genomic s
C 70	18	100.0	942	ABK42958 Genomic s
C 71	18	100.0	942	ABK42958 Genomic s
C 72	18	100.0	942	ABK42958 Genomic s
C 73	18	100.0	942	ABK42958 Genomic s
C 74	18	100.0	942	ABK42958 Genomic s
C 75	18	100.0	942	ABK42958 Genomic s
C 76	18	100.0	942	ABK42958 Genomic s
C 77	18	100.0	942	ABK42958 Genomic s
C 78	18	100.0	942	ABK42958 Genomic s
C 79	18	100.0	942	ABK42958 Genomic s
C 80	18	100.0	942	ABK42958 Genomic s
C 81	18	100.0	942	ABK42958 Genomic s
C 82	18	100.0	942	ABK42958 Genomic s
C 83	18	100.0	942	ABK42958 Genomic s
C 84	18	100.0	942	ABK42958 Genomic s
C 85	18	100.0	942	ABK42958 Genomic s
C 86	18	100.0	942	ABK42958 Genomic s
C 87	18	100.0	942	ABK42958 Genomic s
C 88	18	100.0	942	ABK42958 Genomic s
C 89	18	100.0	942	ABK42958 Genomic s
C 90	18	100.0	942	ABK42958 Genomic s
C 91	18	100.0	942	ABK42958 Genomic s
C 92	18	100.0	942	ABK42958 Genomic s
C 93	18	100.0	942	ABK42958 Genomic s
C 94	18	100.0	942	ABK42958 Genomic s
C 95	18	100.0	942	ABK42958 Genomic s
C 96	18	100.0	942	ABK42958 Genomic s

C	97	14.8	82.2	10332	7	AAC37617	Aac37617	Prokaryote
C	98	14.8	82.2	14985	2	AAT43574	Aat43574	Human box
C	99	14.8	82.2	14985	2	AAV15693	Aav15693	Human bin
C	100	14.8	82.2	20015	5	ABA20740	AbA20740	Human ner
C	101	14.8	82.2	23677	2	AAK16323	AaK16323	Partial h
C	102	14.8	82.2	25701	4	AAI07078	AAI07078	Human rep
C	103	14.8	82.2	25758	4	AAI07077	AAI07077	Human rep
C	104	14.8	82.2	55939	9	ADOC8549	AdOc8549	Mouse Git
C	105	14.8	82.2	55939	9	ADB02869	AdB02869	Mouse Git
C	106	14.8	82.2	55939	9	ADB72707	AdB72707	Mouse Git
C	107	14.8	82.2	73467	7	ABK90695	AbK90695	DNA encod
C	108	14.8	82.2	73467	7	ABK95843	AbK95843	Genomic D
C	109	14.8	82.2	86765	9	ADD14752	Add14752	Human src
C	110	14.8	82.2	110000	4	AAI99682_10	Contiuation (11 c	
C	111	14.8	82.2	110000	4	AAI99683_10	Continuation (11 c	
C	112	14.8	82.2	110000	4	ADB12064_13	Continuation (14 c	
C	113	14.8	82.2	157875	6	ABK99972	AbK99972	Human CAD
C	114	14.8	82.2	349980	6	ABQ81849	Abq81849	Bifidobac
C	115	14.8	82.2	349980	6	ABQ81848	AbQ81848	Bifidobac
C	116	14.4	80.0	247	8	ABX94323	Abx94323	Human bre
C	117	14.4	80.0	360	6	ABY78204	AbY78204	Human ID3
C	118	14.4	80.0	360	6	ABZ35780	Abz35780	Human ID3
C	119	14.4	80.0	360	6	ABX10023	Abx10023	Human ID3
C	120	14.4	80.0	360	6	ABL91745	AbL91745	Human pol
C	121	14.4	80.0	429	8	ACH21548	AcH21548	Human adu
C	122	14.4	80.0	465	8	ACH44238	AcH44238	Human foe
C	123	14.4	80.0	468	4	AAI15262	AAI15262	Probe #51
C	124	14.4	80.0	468	4	AAK05100	AAK05100	Human bra
C	125	14.4	80.0	468	5	AAI04996	AAI04996	Probe #49
C	126	14.4	80.0	468	5	ABS05352	AbS05352	Human gen
C	127	14.4	80.0	475	8	ACH26539	Ach26539	Human adu
C	128	14.4	80.0	481	8	ACH14773	AcH14773	Human adu
C	129	14.4	80.0	495	4	AAI22113	AAI22113	Probe #12
C	130	14.4	80.0	495	4	ABA67192	AbA67192	Human foe
C	131	14.4	80.0	495	4	AAI47408	AAI47408	Probe #15
C	132	14.4	80.0	495	4	ABA49278	AbA49278	Human bre
C	133	14.4	80.0	495	4	ABA34287	AbA34287	Probe #12
C	134	14.4	80.0	495	4	AAK41370	AAK41370	Human bon
C	135	14.4	80.0	495	4	AAK15636	AAK15636	Human bxa
C	136	14.4	80.0	495	4	ABG40961	ABg40961	Human liv
C	137	14.4	80.0	495	5	AAI07811	AAI07811	Probe #78
C	138	14.4	80.0	495	5	ABE15375	ABe15375	Human gen
C	139	14.4	80.0	513	3	AAZ53547	AAz53547	Nelseteria
C	140	14.4	80.0	556	8	ACH42310	AcH42310	Human foe
C	141	14.4	80.0	581	3	AAZ53548	AAz53548	Nelseteria
C	142	14.4	80.0	582	3	AAZ53546	AAz53546	Nelseteria
C	143	14.4	80.0	810	4	AAH20514	AaH20514	B. catyop
C	144	14.4	80.0	810	5	AAF61765	Aaf61765	B. catyop
C	145	14.4	80.0	882	2	AAO44245	Aao44245	HERR-1 ge
C	146	14.4	80.0	982	6	ABO88114	AbO88114	Human ost
C	147	14.4	80.0	982	7			

[illegible]

CC is preferably a phosphorodiamidate-linked morpholino oligonucleotide.
CC Such targeting is effective to inhibit natural mRNA splice processing,
CC produce splice variant mRNAs, and inhibit normal expression of the
CC protein. The present sequence is an antisense sequence described in the
CC exemplification of the invention

XX SQ Sequence 18 BP; 3 A; 6 C; 7 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 18;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGTCTGGC 18
DB 1 CCCGAGAGCAGTCTGGC 18

RESULT 2

AA519107
ID AA519107 standard; DNA; 36 BP.

XX AA519107;

XX 15-MAR-2002 (first entry)

DE Human p53 coding sequence antisense sequence SEQ ID NO: 36.

XX Antisense; splice region; mRNA splice processing inhibition;

KM splice variant; protein expression inhibition; human; HIV-1; rat; ss.

XX Homo sapiens.

XX WO200183740-A2.

XX 08-NOV-2001.

XX 04-MAY-2001; 2001WO-US014410.

XX 04-MAY-2000; 2000US-0202376P.

XX (AVTB-) AVI BIOPHARMA INC.

XX Iversen PL, Hudziak R;

XX WPI; 2002-066533/09.

XX Splice-region antisense composition and method.

XX Claim 37; Page 23; 53pp; English.

XX The present invention relates to antisense compositions targeted to an
XX mRNA sequence for a selected protein, at a region having its 5' end from
XX 1 to about 25 base pairs downstream of a normal splice acceptor junction
XX in the preprocessed mRNA. The antisense compound is RNase-inactive, and
XX is preferably a phosphorodiamidate-linked morpholino oligonucleotide.
XX Such targeting is effective to inhibit natural mRNA splice processing,
XX produce splice variant mRNAs, and inhibit normal expression of the
XX protein. The present sequence is an antisense sequence described in the
XX exemplification of the invention

XX SQ Sequence 36 BP; 6 A; 11 C; 12 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGTCTGGC 18
DB 17 CCCGAGAGCAGTCTGGC 34

RESULT 3

AA519107

ID AAX26511 standard; DNA; 37 BP.

XX AAX26511;

XX 28-MAY-1999 (first entry)

XX WO 9909191 SeqID #13.

XX Cancer; treatment; vector; recombinase gene; transcription factor;
XX selective cell killing; gene therapy; primer; ss.

XX Synthetic.

XX WO9909191-A1.

XX 25-FEB-1999.

XX 02-JUL-1998; 98WO-JP002993.

XX 20-AUG-1997; 97JP-00223651.

XX (DNAV-) DNAMEC RES INC.

XX Yokoi H, Takeda K, Hasegawa M;

XX WPI; 1999-181048/15.

XX Gene expression specific to cells free from specific transcription factor
XX with constructed recombinase expression unit after infecting cells -
XX allowing expression of target gene in gene therapy, particularly in
XX cancer treatment.

XX Example 1; Page 16; 49pp; Japanese.

XX This invention describes a vector containing a recombinase gene which is
XX controlled by (1) a promoter and action of which is in turn dependent on
XX a specific transcription factor and (2) a desired gene to be expressed
XX and two target sequences of the recombinase. Also described in the
XX invention are (1) a host cell for introduction of the vector and (1) an
XX in vitro technique in which killing of cells without the specific
XX transcription factor is selectively performed after the vector is
XX introduced into a host cell by an in vitro technique. The technique is
XX used for gene therapy e.g. in cancer treatment. The products of the
XX invention allow the use of a specific vector specifically and safely,
XX there is little toxicity

XX SQ Sequence 37 BP; 7 A; 13 C; 9 G; 8 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 37;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGTCTGGC 18
DB 30 CCCGAGAGCAGTCTGGC 13

RESULT 4

AAV17739
ID AAV17739 standard; cDNA; 140 BP.

XX AAV17739;

XX 14-AUG-1998 (first entry)

XX Human breast cancer related gene BC532L.

XX L-oncogene; diagnosis; treatment; ovarian cancer; antibody; antisense;

XX ss.

XX Homo sapiens.

XX Key Location/Qualifiers


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FT CDS 4..138
FT /*tag= a
FT /product= "BC532L"
XX
XX
XX WO9807851-A2.
XX
XX PD 26-FEB-1998.
XX
XX PF 22-AUG-1997; 97WO-EP004600.
XX
XX PR 22-AUG-1996; 96CA-02183900.
XX
XX PA (BERG/) BERGMANN J E.
XX (PRED/) PREDDIE E R.
XX
XX PI Bergmann JE, Preddie ER;
XX
XX WPI: 1998-169156/15.
XX
XX P-PSDB; AAW48346.
XX
XX PT Human breast cancer related genes - used for diagnosis, pre-symptomatic
XX detection and therapy of breast and ovarian cancers.
XX
XX PS Claim 2; Fig 1c; 96pp; English.
XX
XX CC Human breast cancer related genes, l-oncogenes (AAV17738-V17753), and the
XX proteins encoded can be used in the diagnosis and treatment of breast and
XX ovarian cancer. Antibodies and multiple antigenic peptide epitopes can be
XX used to detect the presence of the proteins. The antibodies can also be
XX used to block the activity of the proteins. Antisense molecules can be
XX used to prevent expression of the proteins
XX
XX SQ Sequence 140 BP; 29 A; 48 C; 42 G; 21 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTGCGC 18
DB 14 CCCGAGAGCAGCTGCGC 31

RESULT 5
AAQ74245
ID AAQ74245 standard; cDNA; 255 BP.
XX
XX AAQ74245;
XX
XX AC 25-MAR-2003 (revised)
XX DT 02-JUN-1995 (first entry)
XX
XX DE p53 antisense strand cDNA encoding protein BC538.1.
XX
XX KM BC534; BC538; BC538.1; p53 antisense strand; breast cancer; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO9421791-A1.
XX
XX PD 29-SEP-1994.
XX
XX PF 04-MAR-1994; 94WO-EP000651.
XX
XX PR 16-MAR-1993; 93US-00032843.
XX
XX PA (BERG/) BERGMANN J E.
XX (PRED/) PREDDIE E R.
XX
XX PI Bergmann JE, Preddie ER;
XX
XX WPI: 1994-357732/44.
XX
XX P-PSDB; AAW51627.

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XX
XX PR New p53 anti sense proteins - used to develop prods. for the diagnosis,
XX prediction and treatment of breast cancer and related cancers.
XX
XX PS Claim 1; Fig 1E; 46pp; English.
XX
XX CC AAQ74243, AAQ74244 and AAQ74245 are cDNA fragments of the p53 gene
XX antisense strand which encode AAW51625 (BC534), AAW51626 (BC538) and
XX AAW51627 (BC538.1) respectively. These proteins can be used to develop
XX products which can be used in the diagnosis and prediction of breast
XX cancer and other cancers associated with mutations of the p53 gene.
XX These cancers can be treated by providing the patient with an inhibitor
XX of the BC534, BC538 and BC538.1 genes, and the regulatory sequence
XX AAQ74246 (BC53/Reg). (Updated on 25-MAR-2003 to correct PM field.)
XX
XX SQ Sequence 255 BP; 58 A; 82 C; 66 G; 49 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 255;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTGCGC 18
DB 14 CCCGAGAGCAGCTGCGC 31

RESULT 6
AAV17740
ID AAV17740 standard; cDNA; 255 BP.
XX
XX AAV17740;
XX
XX AC 14-AUG-1998 (first entry)
XX
XX DT 14-AUG-1998
XX
XX DE Human breast cancer related gene BC533L.
XX
XX KM l-oncogene; diagnosis; treatment; ovarian cancer; antibody; antisense;
XX ss.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT CDS 3..255
XX FT /*tag= a
XX FT /product= "BC533L"

WO9807851-A2.
XX
XX PD 26-FEB-1998.
XX
XX PF 22-AUG-1997; 97WO-EP004600.
XX
XX PR 22-AUG-1996; 96CA-02183900.
XX
XX PA (BERG/) BERGMANN J E.
XX (PRED/) PREDDIE E R.
XX
XX PI Bergmann JE, Preddie ER;
XX
XX WPI: 1998-169156/15.
XX
XX P-PSDB; AAW48347.
XX
XX PT Human breast cancer related genes - used for diagnosis, pre-symptomatic
XX detection and therapy of breast and ovarian cancers.
XX
XX PS Claim 1; Fig 1e; 96pp; English.
XX
XX CC Human breast cancer related genes, l-oncogenes (AAV17738-V17753), and the
XX proteins encoded can be used in the diagnosis and treatment of breast and
XX ovarian cancer. Antibodies and multiple antigenic peptide epitopes can be
XX used to detect the presence of the proteins. The antibodies can also be
XX used to block the activity of the proteins. Antisense molecules can be
XX used to prevent expression of the proteins

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XX Sequence 255 BP; 58 A; 83 C; 65 G; 49 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 18; DB 2; Length 255;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGAGCTGTGGC 18
 |||||
 DB 14 CCGGAGGAGCTGTGGC 31

RESULT 7
 AAT59673/c
 ID AAT59673 standard; DNA; 800 BP.
 AC AAT59673;
 XX
 DT 07-OCT-1997 (first entry)
 XX
 DE Human p53 gene fragment.
 XX
 KM Target nucleotide sequence; point mutation; analysis;
 KM Criminal investigation; parental determination; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT exon 421..699
 FT /tag= a
 FT /number= 1
 FT /note= "Exon in which possible mutation sites occur"
 FT misc_difference 467
 FT /tag= b
 FT /note= "Wild-type A could be point mutated to T"
 FT misc_difference 605
 FT /tag= c
 FT /note= "Wild-type C could be point mutated to A"
 XX
 PN MO9641001-A1.
 PD 19-DEC-1996.
 XX
 PF 05-JUN-1996; 96WO-US008759.
 XX
 PR 07-JUN-1995; 95US-00472239.
 XX
 PA (ONCO-) ONCOR INC.
 XX
 PI George AL, Bhattachar SK, Nazarenko I;
 DR WPI; 1997-099941/09.
 XX
 PT Analysis of target nucleotide sequence which exists in a first state or
 PT different second state - useful for determination of point mutation(s).
 XX
 PS Disclosure: Page 45-46; 78pp; English.
 XX
 CC A novel method has been produced for analyzing a target nucleotide
 CC sequence. The target sequence having a first segment, a second segment
 CC and a third segment between the first and second, which is formed of at
 CC least one, but less than four different, nucleotide(s) where the third
 CC segment has a nucleotide or nucleotide sequence in a first state or
 CC different second state. The present sequence is a partial human p53 gene
 CC sequence which is used as an example of a target nucleotide sequence. The
 CC method can be used to analyse the entire sequence (portion) of a known
 CC gene and to analyse infectious disease or to determine if a sample is
 CC from a particular source, such as for criminal investigations or parental
 CC determination. Especially the method is used to determine the existence
 CC or absence of mutations consisting of one or a few nucleotides
 CC
 SQ Sequence 800 BP; 148 A; 252 C; 214 G; 186 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 2; Length 800;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGAGCTGTGGC 18
 |||||
 DB 108 CCGGAGGAGCTGTGGC 91

RESULT 8
 AB283767/c
 ID AB283767 standard; cDNA; 1024 BP.
 AC AB283767;
 XX
 DT 14-MAY-2003 (first entry)
 XX
 DE Toxicologically relevant human nucleotide sequence #926.
 XX
 KM Toxicologically relevant gene; toxicological response; gene; ss.
 KM
 OS Homo sapiens.
 XX
 PN WO2003016500-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 16-AUG-2002; 2002MO-US026514.
 XX
 PR 16-AUG-2001; 2001US-0313080P.
 XX
 PA (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
 XX
 PI Neft RE, Dunn RT, Adkins K, Pickett GG, Kier LD, Schmeisler K;
 PI Alen P;
 DR WPI; 2003-268322/26.
 XX
 PT Determining a toxicological response to an agent, useful for screening of
 PT drugs, comprises comparing the expression profile of one or more human
 PT toxic response genes to a reference gene expression profile indicative of
 PT toxicity.
 XX
 PS Claim 1; Page 287; 455pp; English.
 XX
 CC The present invention describes a method (M1) for determining a
 CC toxicological response to an agent, which comprises comparing the
 CC expression profile of one or more human toxic response genes to a
 CC reference gene expression profile indicative of toxicity, and so
 CC determining the presence of a toxic response to the agent. Also
 CC described: (1) an array comprising one or more polynucleotides selected
 CC from the genes corresponding to the partial sequences given in AB282842
 CC to AB284764, or their fragments of at least 20 nucleotides, or homologues
 CC; and (2) determining if a gene putatively identified to be a toxic
 CC response gene plays a role on toxic response pathways by determining the
 CC expression profile of the gene after exposure of cells or a human subject
 CC to a known toxic pharmaceutical or industrial agent, comprising: (a)
 CC exposing cells to an agent or isolating cells from a human subject who
 CC was exposed to an agent; (b) obtaining the test gene expression profile
 CC for a putatively identified toxic response gene after exposure to a known
 CC toxic pharmaceutical or industrial agent; and (c) comparing the test
 CC profile to the expression profile of a gene with a similar function or
 CC comparing the test profile to the expression profile of that gene after
 CC exposure to other known toxic compounds. The methods are useful for
 CC predicting and determining toxicological responses on a cellular, organ
 CC or system level. The arrays comprising the human genes are useful for
 CC toxicological screening of drugs, pharmaceutical compounds and chemicals
 CC
 SQ Sequence 1024 BP; 225 A; 317 C; 263 G; 219 T; 0 U; 0 Other;
 XX
 CC Query Match 100.0%; Score 18; DB 7; Length 1024;
 CC Best Local Similarity 100.0%; Pred. No. 27;
 CC Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KM HSP-90; rheumatoid arthritis; cancer; haematopoietic disorder;
KM T cell lymphoma; B cell lymphoma; chronic myeloid leukaemia; CML;
KM acute myeloid leukaemia; AML; chronic myelomonocytic leukaemia; CMML;
KM acute lymphoblastic leukaemia; ALL; APL; NHL; solid tumour;
KM papillary thyroid carcinoma; Ewing's sarcoma; melanoma; liposarcoma;
KM rhabdomyosarcoma; synovial sarcoma; viral infection; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200269900-A2.
XX
PD 12-SEP-2002.
XX
PF 01-MAR-2002; 2002WC-US006518.
XX
PR 01-MAR-2001; 2001US-022751P.
XX
PA (CONF-) CONFORMA THERAPEUTICS CORP.
XX
PI Fritz LC, Burrows FJ;
XX
DR WPI; 2002-698710/75.
XX
P-PSDB; ABG95119.
XX
PT Treating genetically-defined disease associated with chromosomal
PT aberrations yielding oncogenic fusion proteins, e.g. cell proliferative
PT diseases, involves administering an inhibitor of heat shock protein 90.
XX
PS Disclosure; Page 319-320; 389pp; English.
XX
CC The invention describes a method of treating genetically-defined disease
CC associated with chromosomal aberrations yielding oncogenic fusion
CC proteins (I), treating cancerous cells containing (I) in a heterogeneous
CC cell population, treating proliferative diseases associated with mutant
CC protein or cellular protein isoforms (II) dependent on heat shock protein
CC (HSP)-90, or selectively treating cells expressing (II) involving
CC administering HSP90-inhibitor. The method is useful for treating
CC genetically-defined disease with chromosomal aberration yielding
CC oncogenic fusion protein, treating cancerous cells containing fusion
CC protein in heterogeneous cell population, treating proliferative disease
CC (e.g. rheumatoid arthritis or cancer) associated with mutant protein or
CC cellular protein isoform dependent on heat shock protein (HSP)-90 (e.g.
CC p53), or selectively treating cells expressing mutant protein or cellular
CC protein isoform in a patient heterozygous for (II). The method is useful
CC for treating a disease e.g. haematopoietic disorder such as T or B cell
CC lymphoma, chronic myeloid leukaemia (CML), APL, ALL, NHL, and CMML,
CC or a disease characterised by a solid tumour such as papillary thyroid
CC carcinoma, Ewing's sarcoma, melanoma, liposarcoma, rhabdomyosarcoma and
CC synovial sarcoma. The method is also useful for treating viral
CC infections. This sequence encodes a human oncogenic protein
XX
SQ Sequence 1303 BP; 292 A; 403 C; 348 G; 260 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 6; Length 1303;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCGGAAGGACGCTGGC 18
DB 113 CCCGGAAGGACGCTGGC 96
RESULT 12
ACCA9400/C
ID ACCA9400 standard; cDNA; 1303 BP.
XX
AC ACCA9400;
XX
DT 24-JUN-2003 (first entry)
XX
DE Human p53 encoding cDNA.
XX
KW Human; ATM; p53; ATR; FRAP; FRAP related protein; DNA-PK; DNA-PKcs;

KM DNA dependent protein kinase catalytic subunit; anti-HIV; cytosolic;
KM antiproliferative; antitumour; ataxia-telangiectasia; AIDS; cancer; tumour;
KM postrastis; hyperproliferative disorder; chromosome 17p13.1; gene; ss.
XX
OS Homo sapiens.
XX
PH Key Location/Qualifiers
XX CDS 122..1303
XX FT /*tag= a
XX FT /product= "p53"
XX FT /transl_except= (pos:1232..1234,aa:Ser)
XX FT /note="illegible parts of the nucleotide sequence in the
XX FT figure"
XX
XX GB2362952-A.
XX
PD 05-DEC-2001.
XX
PF 21-AUG-2001; 2001GB-00020368.
XX
PR 16-JUL-1997; 97GB-00014971.
XX
PR 16-JUL-1998; 98GB-00015423.
XX
PA (KUDO-) KUDOS PHARM LTD.
XX
PI Jackson SP, Lakin ND, Smith GCM;
XX
DR WPI; 2003-223383/23.
XX
P-PSDB; ABP97119.
XX
PT Assay for compound affecting DNA binding by ataxia-telangiectasia mutated
PT gene, by bringing into contact the gene, protein with kinase activity,
PT DNA and test compound, and determining binding of the gene and DNA.
XX
PS Disclosure; Fig 7b1-11; 129pp; English.
XX
CC The present invention describes an assay (M1) for a compound able to
CC affect DNA binding by an ataxia-telangiectasia mutated (ATM) protein or a
CC protein having an associated kinase activity. M1 comprises bringing into
CC contact a substance which is ATM or a protein having an associated kinase
CC activity which is able to bind DNA and a test compound, and determining
CC binding of ATM and DNA in the presence of the test compound. Also
CC described: (1) an agent (I) capable of affecting DNA binding by ATM
CC obtained using M1; (2) purifying (M2) ATM or related kinase such as ATR;
CC (3) use of DNA (II) for purifying ATM or ATR; and (4) a substantially
CC pure ATM (III) or ATR (IV). ATM has anti-HIV, cytosolic, antiproliferative
CC and antitumour activities. M1 is useful for assaying for a compound able
CC to affect DNA binding by ATM or a protein having an associated kinase
CC activity. (I) is useful in therapy involving modulating ATM action or in
CC the manufacture of a medicament for modulating ATM action. (II) is useful
CC for purifying ATM or ATR. (I) is also useful for treating humans with
CC ataxia-telangiectasia, AIDS or cancer, for treating or preventing disease
CC states associated with premature and normal aging for regulating immune
CC system function, for inhibiting cell proliferation by activating cell
CC cycle check point arrest in the absence of cellular damage, which may be
CC used in the treatment of tumours, cancer, postrastis and other
CC hyperproliferative disorders, for activating p53 in cells without
CC damaging the cells, for augmenting cancer radiotherapy and chemotherapy,
CC or as adjuncts in cancer radiotherapy and chemotherapy. The present
CC sequence encodes human p53 which is given in the exemplification of the
XX
SQ Sequence 1303 BP; 289 A; 401 C; 344 G; 257 T; 0 U; 12 Other;
Query Match 100.0%; Score 18; DB 7; Length 1303;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCGGAAGGACGCTGGC 18
DB 113 CCCGGAAGGACGCTGGC 96

```
RESULT 13
AAD00088/c
ID AAD00088 standard; DNA; 1307 BP.
XX
XX
AC AAD00088;
XX
DT 31-JUL-2000 (first entry)
XX
DE Human tumour-associated antigen p53 DNA.
XX
KW Human; tumour-associated antigen; p53 protein; DNA-binding domain;
KW dermatological; immunosuppressive; antiinflammatory; autoimmune response;
KW SLE; systemic lupus erythematosus; diagnosis; treatment; prevention; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 126..1307
XX FT /*tag= a
XX FT /product= "p53 protein"
XX
XX WO200023082-A1.
XX
XX 27-APR-2000.
XX
XX 19-OCT-1999; 99WO-US024443.
XX
XX 19-OCT-1998; 98US-0104816P.
XX
XX (YEDA ) YEDA RES & DEV CO LTD.
XX
XX Cohen IR, Rotter V, Erez-Alon N, Herkel J;
XX
XX WPI; 2000-339512/29.
XX
XX P-PSDB; AAY70811.
XX
XX Treatment of systemic lupus erythematosus by down-regulating the
XX autoimmune response to the C-terminal DNA-binding domain of the p53
XX protein by an active compound comprising of antibodies to p53 or
XX fragments of p53.
XX
XX Disclosure: Page 79-81; 87pp; English.
XX
XX The patent discloses a method for the treatment of systemic lupus
XX erythematosus (SLE) by down-regulating the autoimmune response to the C-
XX terminal DNA-binding domain of p53 protein by an active compound
XX comprising C-terminal DNA-binding domain of p53, monoclonal antibodies
XX (Ab1) specific to this domain, monoclonal antibodies (Ab2) specific to
XX Ab1 and peptides based on the complementarity determining region of heavy
XX and light chain of Ab1 and Ab2. The active compound is useful in the
XX diagnosis, prevention and treatment of SLE in humans. The present
XX sequence is a human tumour-associated antigen p53 DNA. Antibodies against
XX the C-terminal DNA-binding domain of the p53 protein can be raised and
XX used for diagnosis and treatment of SLE.
XX
XX Sequence 1307 BP; 293 A; 404 C; 350 G; 260 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 3; Length 1307;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCGAGAGCAGTCTGGC 18
DB 117 CCCGAGAGCAGTCTGGC 100
RESULT 14
ABX15394/c
ID ABX15394 standard; DNA; 1307 BP.
XX
XX ABX15394;
XX
DT 01-MAY-2003 (first entry)
```

```
XX
XX Human p53 DNA.
DE
XX
XX Human; p53; degradation; cervical cancer; tumour; ovarian cancer; glioma;
KW carcinoma; squamous cell carcinoma; lung cancer; pancreatic cancer;
KW leukaemia; lymphoma; neuroblastoma; sarcoma; osteosarcoma; glioblastoma;
KW colon carcinoma; melanoma; choriocarcinoma; breast carcinoma; gene; ds;
KW neuroblastoma; rhabdomyosarcoma; Mdm2; cytostatic; antitumour.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 126..1307
XX FT /*tag= a
XX FT /product= "Human p53"
XX
XX US2002132977-A1.
XX
XX 19-SEP-2002.
XX
XX 07-DEC-2000; 2000US-00732384.
XX
XX 08-DEC-1999; 99US-0169816P.
XX
XX (YUAN/) YUAN Z.
XX
XX (GUJ/) GU J.
XX
XX Yuan Z, Gu J;
XX
XX WPI; 2003-197937/19.
XX
XX P-PSDB; ABG73431.
XX
XX Novel polypeptide that inhibits degradation of endogenous p53 in a
XX mammalian cell, useful for treating cancer, e.g. cervical cancer or a
XX tumor such as sarcoma or carcinoma.
XX
XX Example 2; Page 3; 21pp; English.
XX
XX The invention relates to a substantially pure polypeptide that inhibits
XX degradation of endogenous p53 in a mammalian cell. The polypeptide or a
XX synthetic polypeptide comprising a region of the pure polypeptide is
XX useful for inhibiting degradation of endogenous p53 in a mammalian cell,
XX e.g. in cervical cancer cells or tumour cells selected from sarcoma,
XX carcinoma, squamous cell carcinoma, ovarian cancer, lung cancer,
XX pancreatic cancer, leukaemia, lymphoma, glioma, neuroblastoma,
XX osteosarcoma, colon carcinoma, melanoma, choriocarcinoma, breast
XX carcinoma, glioblastoma, neuroblastoma and rhabdomyosarcoma cells. The
XX cell comprises an Mdm2 amplification or overexpresses Mdm2. A degradation
XX -resistant p53 polypeptide is useful for inhibiting tumour growth, where
XX the tumour is a cervical cancer and comprises a p53 mutation. The
XX polypeptide, and DNA encoding the polypeptide, are useful for treating
XX cancer. This sequence represents DNA encoding the human p53 polypeptide
XX
XX Sequence 1307 BP; 293 A; 404 C; 350 G; 260 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 7; Length 1307;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCGAGAGCAGTCTGGC 18
DB 117 CCCGAGAGCAGTCTGGC 100
RESULT 15
AAT32831/c
ID AAT32831 standard; DNA; 1317 BP.
XX
XX AAT32831;
XX
XX 06-NOV-1996 (first entry)
XX
XX Human p53 tumour suppressor protein gene.
DE
```

```

XX p53 protein; tumour suppressor; tetramerisation domain;
XX chimaeric protein; gene therapy; vector; cell proliferation; cancer;
XX apoptosis; autoimmune disease; immune tolerance; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 136..1317
FT /*tag= a
XX
XX MO9616989-A1.
XX
XX 06-JUN-1996.
XX
XX 27-NOV-1995; 95WO-US015353.
XX
XX 28-NOV-1994; 94US-00347792.
XX 28-APR-1995; 95US-00431357.
XX 01-JUN-1995; 95US-00456623.
XX
XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
XX Halazonetis TD;
XX
XX WPI; 1996-286828/29.
XX
XX P-PSDB; AAM02617.
XX
XX New chimaeric p53 protein with heterologous tetramerisation domain - and
XX related DNA and vectors, useful for treating abnormal cell proliferation,
XX esp. cancer, auto-immune disease, etc.
XX
XX Disclosure; Page 66-68; 123pp; English.
XX
XX A DNA sequence (AA132831) codes for wild-type p53 protein (AAM02617), a
XX sequence-specific DNA binding protein which has tumour suppressor
XX function. p53 regulates cell proliferation and apoptosis and participates
XX in cellular response to DNA damaging agents. It is inactivated in more
XX than half of all human tumours. DNA constructs encoding p53 proteins with
XX altered tetramerisation domains that retain wild-type p53 function can be
XX used in gene therapy to treat abnormal cell proliferation, esp. cancer.
XX or to induce immune tolerance to facilitate transplants and treat
XX autoimmune diseases
XX
XX Sequence 1317 BP; 297 A; 408 C; 350 G; 262 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 2; Length 1317;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCGGAAGGCGAGTCTGGC 18
DB 127 CCCGGAAGGCGAGTCTGGC 110

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FT /product= "human p53"
XX
XX MO9815285-A1.
XX
XX 16-APR-1998.
XX
XX 10-OCT-1997; 97WO-US018807.
XX
XX 10-OCT-1996; 96US-0028193P.
XX
XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
XX Ert1 HCU, Thurin M;
XX
XX WPI; 1998-240594/21.
XX
XX P-PSDB; AAM46858.
XX
XX Pharmaceutical or vaccine comprising DNA encoding p53 and optionally
XX chemokine or cytokine - is useful for treatment and prevention of tumours
XX by inducing protective immune response.
XX
XX Disclosure; Page 51-53; 74pp; English.
XX
XX This is the nucleotide sequence of the human p53 gene, used in the method
XX of the invention involving a pharmaceutical or vaccine comprising DNA
XX encoding p53 and optionally a chemokine or cytokine. The compositions and
XX methods can be used for inducing immune responses to tumour cells which
XX over-express p53 or express mutated p53. They can be used to induce a
XX response to tumour antigens to cause a regression of existing tumours
XX and/or prevent the development of cancers, in e.g. high risk patients
XX
XX Sequence 1317 BP; 297 A; 408 C; 350 G; 262 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 18; DB 2; Length 1317;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCGGAAGGCGAGTCTGGC 18
DB 127 CCCGGAAGGCGAGTCTGGC 110

```

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RESULT 16
AAV18151/c
ID AAV18151 standard; DNA; 1317 BP.
XX
XX AAV18151;
XX
XX 21-AUG-1998 (first entry)
XX
XX Nucleotide sequence of human p53 gene.
XX
XX Human p53 gene; vaccine; chemokine; cytokine; immune response; tumour;
XX mutation; antigen; cancer; ds.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 136..1317
XX /*tag= a
FT

```

```

RESULT 17
AAV21414/c
ID AAV21414 standard; DNA; 1317 BP.
XX
XX AAV21414;
XX
XX 04-AUG-1998 (first entry)
XX
XX Human p53 cDNA homologous probe 3.
XX
XX Probe; gene mapping; RecA-like recombinase; human p53; lambda phage;
XX in situ hybridisation; infectious disease; gene therapy; ds.
XX
XX Synthetic.
XX
XX Homo sapiens.
XX
XX WO9808975-A1.
XX
XX 05-MAR-1998.
XX
XX 29-AUG-1997; 97WO-JF003019.
XX
XX 29-AUG-1996; 96JP-00229061.
XX 26-DEC-1996; 96JP-00347090.
XX
XX (DAIK ) DAIKIN IND LTD.
XX
XX Kigawa K, Yamanaka M, Kusumi K, Mukai E, Ohta K;
XX WPI; 1998-179448/16.
XX

```

PT Targeting DNA by reaction with homologous probe and recombinase - with
 PT addition of heterologous probe to increase efficiency and sensitivity,
 PT useful for in situ hybridisation, gene therapy, cloning of genes, gene
 PT mapping etc.
 XX
 XX Example 1; Page 44; 59pp; English.
 CC The invention provides a method for detecting target DNA in a sample
 CC using RecA-like recombinase and probes homologous to the target DNA.
 CC Addition of heterologous probes was found to increase the sensitivity and
 CC efficiency of detecting the target DNA. In the example given, the target
 CC DNA was the human p53 cDNA which was incorporated in a pHP53B plasmid.
 CC Homologous probes 1-6 (AAV21407, AAV21408, AAV21412, AAV21414-V21416)
 CC containing a partial sequence of the p53 cDNA were used. The heterologous
 CC probes 1-4 (AAV21409-V21411 and AAV21413) corresponded to a partial
 CC sequence of the lambda phage genome. To measure the specificity of
 CC detecting the target DNA, a heterologous double stranded circular DNA
 CC (plasmid vector pUC18) was also used. The method is useful for detecting
 CC the target DNA in cells by in situ hybridisation and to target the DNA in
 CC living cells by in vivo gene targeting, e.g. for gene therapy. The method
 CC is also claimed to be useful for isolating and cloning target genes from
 CC libraries, in gene mapping and for detecting genetic aberrations or
 CC mutations or infectious diseases
 XX
 SQ Sequence 1317 BP; 293 A; 407 C; 359 G; 258 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 2; Length 1317;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCGAGAGCAGTCTGGC 18
 Db 187 CCCGAGAGCAGTCTGGC 170
 RESULT 18
 AAV44695/C
 ID AAV44695 standard; DNA; 1317 BP.
 AC AAV44695;
 XX
 DT 19-OCT-1998 (first entry)
 DE Human wild-type p53 protein encoding DNA.
 XX
 KW Hydrophobic; p53 protein; mutant; oligomerisation domain; dimerisation;
 KW therapeutic agent; biotechnology; tumour suppressor; apoptosis; human;
 KW transplant rejection; autoimmune disease; systemic lupus erythematosus;
 KW rheumatoid arthritis; psoriasis; atherosclerosis; arterial restenosis;
 KW abnormal cell proliferation; interleukin-2 receptor complex;
 KW three-dimensional structure; 3D structure; transmembrane receptor; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT 136..1317
 FT CDS /tag= a
 FT /product= "wild-type p53 protein"
 XX
 PN WO9831703-A1.
 PD 23-JUL-1998.
 PD 15-JAN-1998; 98WO-US000853.
 PF 15-JAN-1998; 98WO-US000853.
 PR 17-JAN-1997; 97US-0035458P.
 XX
 PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
 XX
 PI Halazonectis TD;
 XX
 DR WPI; 1998-414033/35.
 DR P-PSDB; AAW69217.

XX
 PT Altering three-dimensional structure of protein without denaturing it -
 PT by replacing large hydrophobic amino acids with small ones, or vice
 PT versa, used to, e.g. produce p53 proteins with altered oligomerisation
 PT properties.
 XX
 XX Example 1; Page 33-34; 49pp; English.
 CC This DNA encodes a wild-type p53 protein. The invention provides a method
 CC for altering the three-dimensional (3D) structure of a protein, without
 CC denaturing the protein. The method comprises identifying hydrophobic
 CC residues in the protein and classifying the residues as large or small
 CC according to size of the side chain. Mutants in which the hydrophobic
 CC residues have been substituted are produced and they can be analysed for
 CC a change in the 3D structure. The method is applied to non-linear
 CC proteins having a hydrophobic core. A p53 oligomerisation domain can be
 CC altered by this method. Vectors containing nucleic acids encoding a p53
 CC oligomerisation domain and fusion proteins of the p53 oligomerisation
 CC domain with a heterologous domain are useful as therapeutic and
 CC diagnostic agents, in biotechnology and other industrial applications.
 CC Typically altered p53 is useful as tumour suppressor, to induce apoptosis
 CC in proliferating lymphocytes, to prevent transplant rejection, to treat
 CC autoimmune diseases such as systemic lupus erythematosus and rheumatoid
 CC arthritis, and to suppress proliferation in cases of psoriasis,
 CC atherosclerosis and arterial restenosis. They are also used to diagnose
 CC diseases associated with p53 and abnormal cell proliferation. Typical
 CC heterologous proteins are antibodies against Fos or Jun, soluble
 CC interleukin-2 receptor complex (for screening drugs that bind the native
 CC receptor and as therapeutic decoys) and transmembrane receptors. The p53
 CC oligomerisation domain may also be used to induce dimerisation of DNA-
 CC binding proteins, especially c-myc. Altered proteins retain biological
 CC function but have better stability, binding and lower molecular weight
 CC (so enter cells more easily). When expressed from a gene therapy vector,
 CC the altered p53 will not be sequestered into inactive heterodimers by
 CC mutant p53 present in the cells
 XX
 SQ Sequence 1317 BP; 297 A; 408 C; 350 G; 262 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 2; Length 1317;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCCGAGAGCAGTCTGGC 18
 Db 127 CCCGAGAGCAGTCTGGC 110
 RESULT 19
 AAC84597/C
 ID AAC84597 standard; DNA; 1317 BP.
 AC AAC84597;
 XX
 DT 02-APR-2001 (first entry)
 DE Human p53 protein encoding DNA.
 XX
 KW S-phase kinase associated protein; SKP1; SKP2; SKP2-like protein; ZF;
 KW CUL-1; cullin; CDC63; p27; cyclin E; Max; Mad; c-Myc; MDM2; p53; Bax;
 KW Bad; Bcl-2; tumour; cytoskeletal; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT WO200075184-A1.
 FT 14-DEC-2000.
 PD 05-JUN-2000; 2000WO-US015449.
 PF 05-JUN-2000; 2000WO-US015449.
 PR 04-JUN-1999; 99US-0137494P.
 XX
 PA (UYVA) UNIV YALE.
 XX

PI Zhang H, Tsvetkov LM, Kondo T;
 XX WPI; 2001-061703/07.
 DR P-PSDB; AAB348285.
 XX
 PT Modulating polypeptide levels in a cell, diagnosing and treating tumor,
 PT involves altering levels of proteins such as S-phase kinase associated
 PT proteins 1, 2 and cullin/CDC53 proteins.
 XX
 PS Example; Page 97-99; 162pp; English.
 XX
 CC The invention relates to methods of altering the polypeptide levels in a
 CC cell, using proteins selected from S-phase kinase associated proteins 1
 CC and 2 (SKP1, SKP2), SKP2-like proteins (2F) and CUL-1 (a member of the
 CC cullin/ CDC53 family of proteins). The method is useful for altering the
 CC level of p27, cyclin E, Max, Mad, c-Myc, MDM2, p53, Bax, Bad or Bcl-2
 CC polypeptide in a cell. SKP2 and SKP2-like protein levels are useful for
 CC detecting tumours, and in monitoring tumor treatment in a mammal. Agents
 CC that modulate interactions between SKP and target proteins are useful for
 CC treating tumours
 CC
 SQ Sequence 1317 BP; 295 A; 408 C; 352 G; 262 T; 0 U; 0 Other;
 XX
 Query Match 100.0%; Score 18; DB 4; Length 1317;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CCGCGAAGGCGAGTCTGGC 18
 Db 127 CCGCGAAGGCGAGTCTGGC 110
 RESULT 20
 AAD12279/c
 ID AAD12279 standard; cDNA; 1317 BP.
 XX
 AC AAD12279;
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DB Human p53 cDNA.
 XX
 KM Human; gene structure; phenotypic expression; guanosine cofactor;
 KM gemline variation analysis; exon-intron boundary; Tetrahymena RNA; p53;
 KM ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT primer_bind /tag= a
 FT /bound_moiety= "Primer 1a"
 FT 136..138
 FT misc_signal
 FT /tag= b
 FT /note= "Translation start site"
 FT complement(137..156)
 FT primer_bind /tag= c
 FT /bound_moiety= "Primer 2a"
 FT complement(321..344)
 FT primer_bind /tag= d
 FT /bound_moiety= "Primer 3a"
 FT complement(516..535)
 FT primer_bind /tag= e
 FT /bound_moiety= "Primer 4a"
 FT complement(615..634)
 FT primer_bind /tag= f
 FT /bound_moiety= "Primer 5a"
 FT 640..659
 FT primer_bind /tag= g
 FT /bound_moiety= "Primer 5b"
 FT complement(792..811)
 FT primer_bind /tag= h
 FT /bound_moiety= "Primer 6a"

FT primer_bind complement(933..952)
 FT /tag= i
 FT /bound_moiety= "Primer 7a"
 FT 962..981
 FT primer_bind /tag= j
 FT /bound_moiety= "Primer 7b"
 FT 1082..1101
 FT primer_bind /tag= k
 FT /bound_moiety= "Primer 8b"
 FT complement(1124..1143)
 FT primer_bind /tag= l
 FT /bound_moiety= "Primer 8a"
 FT primer_bind complement(1257..1276)
 FT /tag= m
 FT /bound_moiety= "Primer 9a"
 XX
 MO200153529-A2.
 XX
 PD 26-JUL-2001.
 XX
 PF 17-JAN-2001; 2001WO-US001461.
 XX
 PR 20-JAN-2000; 2000US-00488127.
 XX
 PA (GENO-) GENOME THERAPEUTICS CORP.
 XX
 PI Thomann H, Fitzgerald MS;
 XX
 DR WPI; 2001-465380/50.
 XX
 XX Determining structure of genes whose sequence is not known from cDNA, by
 PT sequencing the gene or gene across exon-intron boundaries using evenly
 PT spaced primers comprising nucleic acids that hybridize to the cDNA of
 PT gene.
 XX
 XX Example 2; Fig 2; 81pp; English.
 XX
 PS The present invention relates to a method for determining gene structure
 CC when the genomic sequence is unknown. The method involves sequencing the
 CC gene across exon-intron boundaries using evenly spaced primers or tiled
 CC primers. The tiled primers comprises nucleic acids that hybridize to the
 CC known cDNA sequence of the gene at about 100-300 base intervals and the
 CC gene comprises the template. Gene structure can be determined without the
 CC need to sequence the entire gene. The method provides information
 CC necessary to determine gene structure and phenotypic expression without
 CC the need to sequence entire chromosomal copy of the gene or fragment. The
 CC methods are useful in gemline sequence variation analysis. The method is
 CC also useful for determining the boundaries between regions of nucleic
 CC acids that were separated by intervening sequence, and also for
 CC determining boundaries present in genes containing group 1 type introns
 CC such as Tetrahymena RNA, where self-splicing occurs in the presence of
 CC guanosine cofactor. The present sequence is human p53 cDNA related to the
 CC invention
 XX
 SQ Sequence 1317 BP; 295 A; 408 C; 352 G; 262 T; 0 U; 0 Other;
 XX
 Query Match 100.0%; Score 18; DB 4; Length 1317;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CCGCGAAGGCGAGTCTGGC 18
 Db 127 CCGCGAAGGCGAGTCTGGC 110
 RESULT 21
 AAD43929/c
 ID AAD43929 standard; DNA; 1317 BP.
 XX
 AC AAD43929;
 XX
 DT 13-DEC-2002 (first entry)
 XX


```

DE Human p53 wild-type DNA.
XX
XX Human; p53 protein; transplant rejection; systemic lupus erythematosus;
XX autoimmune disease; rheumatoid arthritis; atherosclerosis; psoriasis;
XX cancer; arterial restenosis; vaccine; gene therapy; protein therapy;
XX immunosuppressant; cytostatic; antiatherosclerotic; gene; ds.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 136. 1317
XX CDS /*tag= a
XX FT /product= "Human p53 wild-type protein"
XX
XX US618062-B1.
XX
XX 14-MAY-2002.
XX
XX 05-MAY-1999; 99US-00305914.
XX
XX 08-MAY-1998; 98US-0084839P.
XX
XX (WIST-) WISTAR INST ANATOMY & BIOLOGY.
XX
XX Halazonetis TD, Stavridi ES;
XX
XX MPI: 2002-462356/49.
XX P-PSDB; AAE26342.
XX
XX Modified p53 protein useful for preventing diagnosing and treating e.g.
XX cancers and psoriasis, comprises a modified p53 tetramerization domain
XX that does not hetero-oligomerize with the native p53 tetramerization
XX domain.
XX
XX Disclosure: Col 13-16; 14pp; English.
XX
XX The present invention relates to novel modified p53 proteins containing a
XX p53 DNA binding domain and a modified p53 tetramerization domain that
XX does not hetero-oligomerize with the native p53 tetramerization domain.
XX Sequences of the invention are useful for the prevention, diagnosis and
XX treatment of diseases associated with inappropriate p53 expression and
XX activity. They are used to treat disorders associated with decreased
XX expression by rectifying mutations or deletions in a patient's genome
XX that affect the activity of p53 by expressing inactive proteins or to
XX supplement the patient's own production of p53. p53 sequences are useful
XX to prevent transplant rejection, to treat autoimmune diseases such as
XX systemic lupus erythematosus, rheumatoid arthritis, cancers, psoriasis,
XX atherosclerosis and arterial restenosis. They are also used as vaccines.
XX Sequences of the invention are used in gene therapy and protein therapy.
XX The present sequence is human p53 wild-type DNA
XX
XX Sequence 1317 BP; 297 A; 408 C; 350 G; 262 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 6; Length 1317;
XX Best Local Similarity 100.0%; Pred. No. 28;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CCCGAGGCGAGCTGTGGC 18
DB 127 CCCGAGGCGAGCTGTGGC 110

```

```

XX
XX 12) locus; 17th chromosome deficient; myeloperoxidase production;
XX antifungal; antiviral; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FH 215. .1396
XX CDS /*tag= a
XX FT 539. .541
XX FT /*tag= b
XX FT /note= "TTV to TTG mutation resulting in Phe to Leu
XX mutation in resultant protein"
XX 936. .938
XX FT /*tag= c
XX FT /note= "CGG to CAG mutation resulting in Arg to Gln
XX mutation in resultant protein"
XX 1031. .1033
XX FT /*tag= d
XX FT /note= "CGT to CAT mutation resulting in Arg to His
XX mutation in resultant protein"
XX 1316. .1318
XX FT /*tag= e
XX FT /note= "CAC to CGC mutation resulting in His to Arg
XX mutation in resultant protein"
XX
XX JP09206070-A.
XX
XX 12-AUG-1997.
XX
XX 31-JAN-1996; 96JP-00037400.
XX
XX 31-JAN-1996; 96JP-00037400.
XX
XX (SRLS-) SRL KK.
XX
XX MPI: 1997-460745/43.
XX P-PSDB; AAW25155.
XX
XX Cell line derived from leukaemic human bone marrow cells - used for the
XX production of myeloperoxidase which has antifungal and antiviral
XX activity.
XX
XX Disclosure: Page 4-6; 6pp; Japanese.
XX
XX AAT79880 is a DNA sequence encoding a p53 mutant protein. The DNA can be
XX found in a new cell line CMC-1 (FERM P-1507), which was derived from a
XX bone marrow cell of a patient with acute myelocytic leukaemia. The cell
XX line has the following characteristics: (a) a chromosomal (8; 21) locus;
XX (b) is deficient in one of 17th chromosomes; and (c) has mis-sense
XX mutations on codons 248 and 368 of the p53 gene. The features table shows
XX these mutations as tags c and e. Mutations shown by tags b and d are not
XX explained in the specification. The cell line is used for production of
XX myeloperoxidase (MPO) which has anti-fungal and anti-viral activity or as
XX a control for detection of the (8; 21) locus in studying acute bone
XX marrow leukemia. MPO can be supplied in a large amount as opposed to
XX conventional production of MPO from blood as the starting material
XX
XX Sequence 1760 BP; 401 A; 512 C; 461 G; 386 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 2; Length 1760;
XX Best Local Similarity 100.0%; Pred. No. 28;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CCCGAGGCGAGCTGTGGC 18
DB 206 CCCGAGGCGAGCTGTGGC 189

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RESULT 23
AAX75765/c
ID AAX75765 standard; DNA; 1760 BP.
XX
XX AAX75765;
AC

```

XX 22-JUL-1999 (first entry)
DT
XX
XX Human p53 cellular tumour antigen DNA.

XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
KW neurofilament-F; presenilin 1; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; NMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A; ss.

XX Homo sapiens.

XX WO9845322-A2.

XX 15-OCT-1998.

XX 02-APR-1998; 98WO-IB000705.

XX 10-APR-1997; 97US-0043163P.

XX (ROYA-) ROYAL NETHERLANDS ACADEMY OF SCI.

XX (UYRO-) UNIV ROTTERDAM ERASMUS.

XX (UYUT-) RIKSUNIV UTRECHT.

XX Van Leeuwen FW, Grosveld FG, Burbach JPH.

XX WPI; 1998-609901/51.

XX Diagnosing disease by detecting frameshift mutations in RNA or

XX corresponding protein mutations - used to diagnose cancer and

XX neurological diseases, particularly Alzheimer's disease, and also for

XX treatment and prevention with specific ribozymes or wild-type RNA.

XX Disclosure; Fig 14; 258pp; English.

XX This invention describes a novel method for the diagnosis of a disease

XX caused by, or associated with, an RNA molecule that has a frameshift

XX mutation. The method is used to diagnose age-related diseases, especially

XX cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's

XX disease, Down's syndrome, myotonic dystrophy, Huntington's disease, II

XX multiple sclerosis, alcoholic liver disease, diabetes mellitus type II

XX and many others listed) or susceptibility to these disorders. The method

XX allows a definitive diagnosis of Alzheimer's disease in living patients,

XX at an early stage. It is based on the observation that disease may be

XX caused by mutations in RNA rather than DNA. The invention describes the

XX beta-amyloid precursor protein (beta-APP), the microtubule associated

XX proteins tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule

XX associated protein 2 (MAP2), neurofilament-L, neurofilament-M,

XX neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic

XX protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma

XX 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group

XX protein-C (NMGP-C) and neuroendocrine specific protein A. This sequence

XX encodes the wild type and mutant protein fragments represented in

XX AAY1054-Y21103

XX Sequence 1760 BP; 401 A; 513 C; 460 G; 386 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 18; DB 2; Length 1760;

XX Best Local Similarity 100.0%; Pred. No. 28;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 CCCGGAAGGCAAGTCTGGC 18

XX DB 206 CCCGGAAGGCAAGTCTGGC 189

RESULT 24
AADS4029/c
ID AADS4029 standard; DNA; 1760 BP.

XX AADS4029;

XX 17-JUN-2003 (first entry)

XX Human colon cancer-associated polypeptide gene, CO-13 (P53).

XX Human; colon cancer-associated polypeptide; immune response; therapy;

XX colon cancer; gene; ds.

XX Homo sapiens.

XX Location/Qualifiers

XX Key 215..1273

XX CDS /tag= a

XX /product= "Human colon cancer-associated polypeptide"

XX /transl_except= (pos:440..442, aa:Xaa)

XX /transl_except= (pos:502..505, aa:Val)

XX /note= "Xaa corresponds to any amino acid"

XX WO200290986-A1.

XX 14-NOV-2002.

XX 02-MAY-2002; 2002WO-US013994.

XX 04-MAY-2001; 2001US-00849602.

XX (LUDW-) LUDWIG INST CANCER RES.

XX (CORR) CORNBELL RES FOUNDR INC.

XX Chen Y, Old LJ, Scanlan MJ, Stockert E,

XX WPI; 2003-112003/10.

XX P-PSDB; AAE35350.

XX Diagnosing colon cancer in a subject comprises identifying colon cancer-

XX associated polypeptides as antigens that elicit immune response in colon

XX cancer.

XX Claim 1; Page 83-84; 122pp; English.

XX The invention relates to a method for diagnosing colon cancer in a

XX subject which comprises identifying colon cancer-associated polypeptides

XX as antigens that elicit immune response in colon cancer. The method is

XX useful for diagnosing, determining onset, progression, or regression of

XX colon cancer in a subject, or for selecting a course of treatment of a

XX subject having or suspected of having colon cancer. The colon cancer-

XX associated polypeptides are useful as markers for diagnosing colon

XX cancer, and for following the course of treatment of colon cancer. The

XX present sequence is human colon cancer-associated polypeptide gene

XX Sequence 1760 BP; 400 A; 513 C; 461 G; 386 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 18; DB 7; Length 1760;

XX Best Local Similarity 100.0%; Pred. No. 28;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 1 CCCGGAAGGCAAGTCTGGC 18

XX DB 206 CCCGGAAGGCAAGTCTGGC 189

XX RESULT 25

XX ABA00952/c

XX ID ABA00952 standard; cDNA; 1760 BP.

XX ABA00952;

XX 16-MAY-2003 (first entry)

```

XX DE Human p53 ORF and surrounding sequences.
XX XX
XX KW Gene; screening; silent information regulator 2; Sir2; deacetylation;
XX KW transcription factor; modulator; p53; DNA repair; apoptosis; oncogenesis;
XX KW gene silencing; senescence; cancer; aging; ionizing radiation; ss.
XX OS
XX OS Homo sapiens.
XX PH
XX PH Key Location/Qualifiers
XX FT CDS 215..1396
XX FT /tag=a
XX FT /product="p53"
XX PN
XX PN WO2003004621-A2.
XX PD
XX PD 16-JAN-2003.
XX XX
XX PF 08-JUL-2002; 2002MO-US021461.
XX XX
XX PR 06-JUL-2001; 2001US-0303370P.
XX PR 06-JUL-2001; 2001US-0303456P.
XX PR 05-JUL-2002; 2002US-00303456.
XX PA
XX PA (ELIX-) ELIXIR PHARM INC.
XX PI
XX PI Guarente L, Vaziri H, Imai S, Gu W,
XX XX
XX DR WPI; 2003-210354/20.
XX DR P-PSDB; AAG79917.
XX XX
XX PT Screening for modulators of silent information regulator 2 (Sir2) protein
XX PT for treating cancer and aging, comprises determining if the compound
XX PT modulates Sir2-mediated deacetylation of the transcription factor.
XX XX
XX PS Disclosure; Fig 14; 93bp; English.
XX XX
XX CC The sequences given in ABA00951-59 encode proteins which were used in the
XX CC method of the invention for the screening of a compound. The method
XX CC comprises determining if the compound modulates silent information
XX CC regulator 2 (Sir2) interaction with a transcription factor or Sir2-
XX CC mediated deacetylation of a transcription factor in a reaction mixture
XX CC comprising Sir2, a transcription factor and the compound. The method is
XX CC useful for screening compounds that modulate cellular and organismal
XX CC processes. Modulators of Sir2 and/or p53 activity are useful in
XX CC modulating various cellular processes, e.g. repair of DNA damage,
XX CC apoptosis, oncogenesis, gene silencing and senescence. Such modulators
XX CC are also useful for treating cancer and aging, or for treating a cell
XX CC that has been exposed to ionizing radiation
XX CC
XX SQ Sequence 1760 BP; 401 A; 513 C; 460 G; 386 T; 0 U; 0 Other;

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Query Match 100.0%; Score 18; DB 7; Length 1760;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCCGGAAGGCACTTGGC 18
DB 206 CCCGGAAGGCACTTGGC 189

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RESULT 26
ADD22450/c
ID ADD22450 standard; DNA; 2451 BP.
XX
XX AC ADD22450;
XX XX
XX DT 15-JAN-2004 (first entry)
XX XX
XX DE HLA-B46 T cell recognised tumour antigenic polypeptide, SEQ No 100.
XX XX
XX KW tumour antigenic peptide; cancer; vaccine; cytostatic; cytotoxic T cell;
XX KW colon; mouth; lung; prostatic; gynecological; human; gene; ds.

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XX OS Homo sapiens.
XX XX
XX PN JP2003111595-A.
XX XX
XX PD 15-APR-2003.
XX XX
XX PF 24-JUN-2002; 2002JP-00183603.
XX PF
XX PR 25-JUN-2001; 2001JP-00191974.
XX PR
XX PA (ITOY) ITO Y.
XX XX
XX DR WPI; 2003-611129/58.
XX XX
XX PT Novel tumor antigenic peptide or polypeptide useful for inducing
XX PT cytotoxic T cells or for treating cancer such as colon, mouth, lung,
XX PT prostatic or gynecological cancer.
XX XX
XX PS Claim 10; SEQ ID NO 100; 98bp; Japanese.
XX XX
XX CC The invention relates to a novel tumor antigenic peptide or polypeptide
XX CC comprising a sequence selected from 99 sequences fully defined in the
XX CC specification. The tumour antigenic peptide or polypeptide comprises a
XX CC sequence selected from 99 sequences fully defined in the specification,
XX CC where the tumour antigenic peptide preferably has a sequence of Glu-Pro-
XX CC Pro-Leu-Ser-Gln-Glu-Ile-Phe, and the polypeptide preferably has a
XX CC sequence comprising 393 amino acids fully defined in the specification.
XX CC The invention further provides a cancer vaccine comprising a tumour
XX CC antigenic peptide or polypeptide, which has cytostatic activity. A tumour
XX CC antigenic peptide, polypeptide, its encoding polynucleotide, a
XX CC hybridising polynucleotide, a recombinant vector containing the
XX CC polynucleotide, a host transformed with the vector or an antibody are
XX CC useful for screening for compounds that interact with the tumour
XX CC antigenic peptide, the polypeptide or its encoding polynucleotide and
XX CC increases the expression of the tumour antigenic peptide, the polypeptide
XX CC or polynucleotide. The tumour antigenic peptide or the polypeptide is
XX CC useful for inducing cytotoxic T cells. The tumour antigenic peptide
XX CC vaccine is useful for treating cancer such as colon, mouth, lung,
XX CC prostatic or gynecological cancer. The invention also provides a
XX CC pharmaceutical composition useful for treating cancer. The tumour
XX CC antigenic peptide or the polypeptide is useful as an antigen to create
XX CC antibodies. This polynucleotide sequence represents the DNA encoding one
XX CC of the human tumour antigenic polypeptides of the invention.
XX XX
XX SQ Sequence 2451 BP; 537 A; 697 C; 592 G; 625 T; 0 U; 0 Other;

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```

Query Match 100.0%; Score 18; DB 9; Length 2451;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 CCCGGAAGGCACTTGGC 18
DB 55 CCCGGAAGGCACTTGGC 38

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RESULT 27
AAS65699/c
ID AAS65699 standard; cDNA; 2600 BP.
XX
XX AC AAS65699;
XX XX
XX DT 13-FEB-2002 (first entry)
XX XX
XX DE DNA encoding novel human diagnostic protein #1503.
XX XX
XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX XX
XX OS Homo sapiens.
XX XX
XX PN WO200175067-A2.
XX XX

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PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Dmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG01512.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 1503; 103bp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2600 BP; 562 A; 741 C; 641 G; 656 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 5; Length 2600;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTGGC 18
DB 206 CCCGAGAGCAGCTGGC 189

RESULT 28
AAS67409/C
ID AAS67409 standard; cDNA; 2605 BP.
XX
AC AAS67409;
XX
DT 13-FEB-2002 (first entry)

XX DNA encoding novel human diagnostic protein #3213.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
XX food supplement; medical imaging; diagnostic; genetic disorder; ss.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US008631.
XX
PR 31-MAR-2000; 2000US-00540217.
XX
PR 23-AUG-2000; 2000US-00649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Dmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR P-PSDB; ABG03222.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 1; SEQ ID NO 3213; 103bp; English.
XX
CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activity. The
CC polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
CC coding sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 2605 BP; 558 A; 740 C; 644 G; 663 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 5; Length 2605;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTGGC 18
DB 206 CCCGAGAGCAGCTGGC 189

RESULT 29
ABA09379/C
ID ABA09379 standard; cDNA; 397 BP.
XX
AC ABA09379;
XX
DT 11-JAN-2002 (first entry)

XX Human p53 homologue-encoding cDNA, SEQ ID NO:1155.

XX Human; cytokine; cell proliferation; cell differentiation; growth factor;
XX haematopoiesis regulation; tissue growth; immunomodulator; activin;
XX inhibin; chemotaxis; chemokinesis; thrombolytic; oncogenesis;
XX proliferation; metastasis; cancer; tumour; haematopoietic disorder;
XX myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
XX chronic inflammatory condition; proliferative retinopathy;
XX atherosclerosis; coronary heart disease; arterial ischaemia;
XX bone disorder; osteoporosis; vascular growth disorder;
XX tissue regeneration; wound healing; infection; immune disorder;
XX cell culture; drug screening; gene therapy; anti-inflammatory;
XX antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;

ABK42958/c
ID ABK42958 standard; DNA; 942 BP.
XX
AC ABK42958;
XX
DT 21-MAY-2002 (first entry)
XX
DE Genomic sequence #857 encoding novel human connective tissue polypeptide.
XX
KW Human; connective tissue related disorder; cancer; gene therapy;
XX Cystostatic; gene; ds.
XX Homo sapiens.
XX WO200155343-A1.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001322.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216889P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218292P.
PR 26-JUL-2000; 2000US-0220963P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225278P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229511P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0231968P.
PR 12-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
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PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-565190/63.
XX
XX Nucleic acid encoding novel connective tissue associated polypeptides,
PT used in diagnosing, preventing, treating or ameliorating a disorder such
PT as cancer or rheumatoid arthritis.
XX
XX
XX Disclosure; SEQ ID NO 1845; 673pp; English.
XX
XX The present invention relates to the isolation of novel human connective
CC tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide
CC (cDNA and genomic) sequences encoding them. The sequences of the
CC invention are useful in the diagnosis, treatment, prevention and/or
CC prognosis of diseases associated with connective tissue(s), including
CC cancer. The polynucleotide sequences of the invention are also useful in
CC gene therapy. AAU42102-AAU43116 represent genomic sequences encoding the
CC novel human connective tissue related polypeptides. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 942 BP; 200 A; 251 C; 240 G; 251 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 942;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGGAGGCACTGTGC 18
Db 58 CCCGGAGGCACTGTGC 41

RESULT 32
ABK42959/C
ID ABK42959 standard; DNA; 942 BP.
XX
XX ABK42959;
AC
XX 21-MAY-2002 (first entry)
DT
XX
XX Genomic sequence #858 encoding novel human connective tissue polypeptide.
DE
XX Human; connective tissue related disorder; cancer; gene therapy;
KM Cytostatic; gene; ds.
XX
XX Homo sapiens.
PN WO200155343-A1.
PN
PD 02-AUG-2001.
PD
PF 17-JAN-2001; 2001WO-US001322.
PF
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XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
DR	WPI, 2001-565190/63.	
XX		
XX		
PT	Nucleic acid encoding novel connective tissue associated polypeptides,	
PT	used in diagnosing, preventing, treating or ameliorating a disorder such	
PT	as cancer or rheumatoid arthritis.	
XX		
PS	Disclosure; SEQ ID NO 1846; 673pp; English.	
XX		
CC	The present invention relates to the isolation of novel human connective	
CC	tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide	
CC	(cDNA and genomic) sequences encoding them. The sequences of the	

Query Match	91.1%	Score 16.4	DB 4	Length 942
Best Local Similarity	94.4%	Pred. No. 1.7e+02		
Matches 17	Conservative 0	Mismatches 1	Indels 0	Gaps 0
1	CCCCGAGGCACTCTGTC	18		
58	CCCCGAGGCACTCTGTC	41		
<p>RESULT 33</p> <p>ADB61115/c</p> <p>ID ADB61115 standard; DNA; 942 BP.</p> <p>AC ADB61115;</p> <p>DT 04-DEC-2003 (first entry)</p> <p>DE Connective tissue related genomic DNA #858.</p> <p>XX</p> <p>XX cytostatic; neuroprotective; nootropic; antiparkinsonian; cardiovascular;</p> <p>XX antiatherosclerotic; immunosuppressive; antihemagic; antiarthritis;</p> <p>XX antiinflammatory; antiallergic; antihemagic; dermatological;</p> <p>XX nephrotropic; virocidic; fungicide; antibacterial; antiparasitic;</p> <p>XX gene therapy; ds; connective tissues disorder; rheumatoid arthritis;</p> <p>XX systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer;</p> <p>XX Alzheimer's disease; neoplasia; leukaemia; neurodegenerative disorder;</p> <p>XX Alzheimer's disease; Parkinson's disease; cardiovascular disease;</p> <p>XX atherosclerosis; myocarditis; cardiopulmonary bypass complication;</p> <p>XX autoimmune disease; multiple sclerosis; allergic reaction; asthma;</p> <p>XX rhinitis; eczema; inflammatory condition; Crohn's disease; nephritis;</p> <p>XX gastrointestinal disorder; inflammatory bowel disease;</p> <p>XX organ transplant rejection; immune system disorder; Bruton's disease;</p> <p>XX X-linked lymphoproliferative syndrome;</p> <p>XX B-cell lymphoproliferative disorder; HIV; AIDS; infection;</p> <p>XX chromosome identification; chromosome mapping;</p> <p>XX connective tissue related polynucleotide; gene; ds.</p> <p>XX Homo sapiens.</p> <p>XX US2003054375-A1.</p> <p>XX</p> <p>XX 20-MAR-2003.</p> <p>XX</p> <p>XX 07-MAR-2002; 2002US-00092154.</p> <p>XX</p> <p>XX 31-JAN-2000; 2000US-0179065P.</p> <p>XX 04-FEB-2000; 2000US-0180628P.</p> <p>XX 24-FEB-2000; 2000US-0184664P.</p> <p>XX 02-MAR-2000; 2000US-0186350P.</p> <p>XX 16-MAR-2000; 2000US-0189874P.</p> <p>XX 17-MAR-2000; 2000US-0190076P.</p> <p>XX 18-APR-2000; 2000US-0198122P.</p> <p>XX 19-MAY-2000; 2000US-0205125P.</p> <p>XX 07-JUN-2000; 2000US-0209467P.</p> <p>XX 28-JUN-2000; 2000US-0214866P.</p> <p>XX 30-JUN-2000; 2000US-0215135P.</p> <p>XX 07-JUL-2000; 2000US-0216647P.</p> <p>XX 11-JUL-2000; 2000US-0217487P.</p> <p>XX 11-JUL-2000; 2000US-0217496P.</p> <p>XX 14-JUL-2000; 2000US-0218290P.</p> <p>XX 26-JUL-2000; 2000US-0220963P.</p>				

CC (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass
CC complications), autoimmune diseases (e.g. systemic lupus erythematosus,
rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.

Query Match 91.1%; Score 16.4; DB 8; Length 942;
Best Local Similarity 94.4%; Pred. No. 1.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGAGGCGAGTGTGGC 18
DB 58 CCCGAGGCGAGTGTGTC 41

RESULT 34

ID ADB6114/c
ADB6114 standard; DNA, 942 BP.

AC ADB6114;

DT 04-DEC-2003 (first entry)

XX Connective tissue related genomic DNA #857.

XX cyostatic; neuroprotective; noctropic; antiparkinsonian; cardiovascular;
XX antiarteriosclerotic; immunosuppressive; antirheumatic; antiarthritic;
XX antiinflammatory; antiallergic; antiasthmatic; dermatological;
XX nephrotoxic; virucide; fungicide; antibacterial; antiparasitic;
XX gene therapy; ds; connective tissues disorder; rheumatoid arthritis;
XX systemic lupus erythematosus; scleroderma; Sjogren's syndrome; cancer;
XX cancer metastasis; neoplasia; leukaemia; neurodegenerative disorder;
XX Alzheimer's disease; Parkinson's disease; cardiovascular disease;
XX atherosclerosis; myocarditis; cardiopulmonary bypass complication;
XX autoimmune disease; multiple sclerosis; allergic reaction; asthma;
XX rinitis; eczema; inflammatory condition; Crohn's disease; nephritis;
XX gastrointestinal disorder; inflammatory bowel disease;
XX organ transplant rejection; immune system disorder; Britton's disease;
XX X-linked lymphoproliferative syndrome;
XX B-cell lymphoproliferative disorder; HIV; AIDS; infection;
XX chromosome identification; chromosome mapping;
XX connective tissue related polynucleotide; gene; ds.

OS Homo sapiens.

XX US2003054375-A1.

XX 20-MAR-2003.

PF 07-MAR-2002; 2002US-00092154.

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PR 11-JUL-2000; 2000US-0217496P.
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 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 05-DEC-2000; 2000US-0255179P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 PR 17-JAN-2001; 2001US-00764847.
 XX
 PA (HUMA-) HUMAN GENOME SCT INC.
 XX
 PI Rosen CA, Ruben SM, Barash SC;
 XX
 DR WPI: 2003-634869/60.
 XX
 DR P-PSDB; ADS9710.
 XX
 PT New connective tissue-related polypeptides and polynucleotides, useful
 PT for treating, preventing and/or prognosing e.g. disorders of connective
 PT tissue, (e.g. rheumatoid arthritis), cancers, cancer metastases and/or
 XX neoplasias.
 XX
 PS Disclosure; SEQ ID NO 1845; 248bp; English.
 CC
 CC The invention describes an isolated nucleic acid molecule (I), which
 CC comprises a sequence that is at least 95 % identical to a connective
 CC tissue-related polynucleotide encoding connective tissue antigens (CTA).
 CC The polypeptide or polynucleotide is useful for preventing, treating, or
 CC ameliorating medical conditions in a mammal. The connective tissue
 CC polypeptides, polynucleotides and antibodies are particularly useful for
 CC treating, preventing and/or prognosing disorders of connective tissues
 CC (e.g. rheumatoid arthritis, discoid and systemic lupus erythematosus),
 CC scleroderma, or Sjogren's syndrome), cancers, cancer metastases and/or
 CC neoplasias (e.g. leukaemia), neurodegenerative disorders (e.g.
 CC Alzheimer's disease, or Parkinson's disease), cardiovascular diseases
 CC (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass
 CC complications), autoimmune diseases (e.g. systemic lupus erythematosus,
 CC rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.

QY 1 CCGGAGGCGAGTGTGCG 18
 Db 58 CCGGAGGCGAGTGTGTC 41
 RESULT 35
 AAH23072/C
 ID AAH23072 standard; DNA; 1866 BP.
 XX
 AC AAH23072;
 DT 17-SEP-2001 (first entry)
 DE Osteoarthritis tissue-derived nucleic acid sequence #2.
 XX
 KM Osteoarthritis; infectious disorder; Crohn's disease; sepsis; human;
 KM wound healing; osteopathic; anti-arthritis; anti-inflammatory; vulnerary;
 KM antibacterial; anti-allergic; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200153531-A2.
 XX
 PD 26-JUL-2001.
 XX
 PF 18-JAN-2001; 2001WO-US000016.
 XX
 PR 18-JAN-2000; 2000US-0176523P.
 XX
 PA (PHAA) PHARMACIA CORP.
 XX
 PI Philpard D, Vasanthakumur G, Dotson S, Ma X;
 XX
 DR WPI: 2001-451914/48.
 XX
 PT Substantially purified protein, polypeptide or their fragments, used to
 PT identify a biologically active compound or composition and treat
 PT mammalian osteoarthritis.
 XX
 PS Claim 1; Page 90-91; 144bp; English.
 XX
 SQ Sequence 1986 BP; 603 A; 410 C; 348 G; 625 T; 0 U; 0 Other;
 CC
 CC Sequences AAH23071-23152 represent nucleic acid sequences derived from
 CC osteoarthritis tissues. The sequences are useful as probes and for the
 CC diagnosis or prognosis of mammalian osteoarthritis. The polynucleotides
 CC and polypeptides of the invention are useful for generating diagnostic
 CC reagents, as targets for small molecule drug development, generation of
 CC therapeutic, and cloning genes. Specific antibodies are used to generate
 CC enzyme linked immunosorbent assays for detection of osteoarthritis. The
 CC invented molecules can be used to treat osteoarthritis or to analyse the
 CC disease-modifying activity of osteoarthritis drugs. Other disorders
 CC treatable using the nucleic acid sequences include atopic, inflammatory
 CC and infectious disorders e.g. Crohn's disease and sepsis, and wound
 CC healing
 XX
 XX
 QY 1 CCGGAGGCGAGTGTGCG 18
 Db 893 CCGGAGGCGAGTGTGCG 876
 RESULT 36
 AAQ72979
 ID AAQ72979 standard; CDNA; 140 BP.
 XX
 AC AAQ72979;
 XX
 DT 30-JUN-1995 (first entry)

```

XX DE p53 human tumour antigen antisense cDNA.
XX KM p53 human tumour antigen; antisense breast cancer therapy; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT CDS 4..138
XX FT /*tag= a
XX CA2090879-A.
XX PN
XX PD 04-SEP-1994.
XX PF 03-MAR-1993; 93CA-02090879.
XX PR 03-MAR-1993; 93CA-02090879.
XX PA (PRED/) PREDDIE R E.
XX PI Predlie RE, Bergmann JE;
XX DR WPI: 1994-333671/42.
XX DR P-PSDB; AAR62645.
XX PT Novel reconstructed cDNA's and encoded proteins - are antisense to human
XX PS tumour antigen p53 gene, useful to provide breast cancer therapy.
XX PS Claim 1; Fig 1; 7pp; English.
XX CC AAQ72979 which encodes AAR62645 is the antisense strand to a p53 gene
XX CC human tumour antigen. In healthy women expression of AAR62645 is
XX CC repressed by the normal wild type p53 gene, however mutations in this
XX CC gene could permit the expression of this antisense protein, which may
XX CC lead to the development of breast cancer. Therefore AAR62645 can be used
XX CC in the development of humanised antibodies against breast cancer, which
XX CC due to AAR62645's non-expression in healthy women, should have no side
XX CC effects
SQ Sequence 140 BP; 30 A; 46 C; 44 G; 20 T; 0 U; 0 Other;

Query Match 88.9%; Score 16; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGAAGGCGAGTCTGGC 18
DB 16 CGAAGGCGAGTCTGGC 31

RESULT 37
AAQ74244
ID AAQ74244 standard; cDNA; 140 BP.
XX AC
XX AC AAQ74244;
XX DT 25-MAR-2003 (revised)
XX DT 02-JUN-1995 (first entry)
XX DE p53 antisense strand cDNA encoding protein BC538.
XX KM BC534; BC538; BC538.1; p53 antisense strand; breast cancer; ss.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT misc_difference 7..9
XX FT /*tag= a
XX FT /transl_except= Ala
XX FT misc_difference 10..12
XX FT /*tag= b
XX FT /transl_except= Val

```

```

FT FT misc_difference 13..15
FT FT /*tag= c
FT FT /transl_except= Thr
XX PN WO9421791-A1.
XX PD 29-SEP-1994.
XX PF 04-MAR-1994; 94WO-EP000651.
XX PR 16-MAR-1993; 93US-00032843.
XX PA (BERG/) BERGMANN J E.
XX PA (PRED/) PREDDIE R E.
XX PI Bergmann JE, Predlie RE;
XX DR WPI: 1994-357732/44.
XX DR P-PSDB; AAR51626.
XX PT New p53 anti sense proteins - used to develop prods. for the diagnosis,
XX PS prediction and treatment of breast cancer and related cancers.
XX PS Claim 1; Fig 1C; 46pp; English.
XX CC AAQ74243, AAQ74244 and AAQ74245 are cDNA fragments of the p53 gene
XX CC antisense strand which encode AAR51625 (BC534), AAR51626 (BC538) and
XX CC AAR51627 (BC538.1) respectively. These proteins can be used to develop
XX CC products which can be used in the diagnosis and prediction of breast
XX CC cancer and other cancers associated with mutations of the p53 gene.
XX CC These cancers can be treated by providing the patient with an inhibitor
XX CC of the BC534, BC538 and BC538.1 genes, and the regulatory sequence
XX CC AAQ74246 (BC53/reg). (Updated on 25-MAR-2003 to correct FN field.)
SQ Sequence 140 BP; 30 A; 46 C; 44 G; 20 T; 0 U; 0 Other;

Query Match 88.9%; Score 16; DB 2; Length 140;
Best Local Similarity 100.0%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGAAGGCGAGTCTGGC 18
DB 16 CGAAGGCGAGTCTGGC 31

RESULT 38
AAA70021
ID AAA70021 standard; cDNA; 184 BP.
XX AC
XX AC AAA70021;
XX DT 07-NOV-2000 (first entry)
XX DE Human ovarian carcinoma antigen polynucleotide SEQ ID NO:332.
XX KM Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
XX KM tumour antigen; identification; cytostatic; gene therapy; vaccine; ss.
XX OS Homo sapiens.
XX PN WO200036107-A2.
XX PD 22-JUN-2000.
XX PF 17-DEC-1999; 99WO-US030270.
XX PR 17-DEC-1998; 99US-00215681.
XX PR 17-DEC-1998; 98US-00216003.
XX PR 23-JUN-1999; 99US-00338933.
XX PR 24-SEP-1999; 99US-00404879.
XX PA (CORI-) CORIXA CORP.

```

PI Mitcham JL, King GE, Algate PA, Frudakis TN;
DR WPI; 2000-431589/37.
XX
PT Immunogenic portion of an ovarian carcinoma protein and the nucleic acid
PT encoding it, useful for the diagnosis, prevention and treatment of
PT cancer, preferably ovarian cancer.
XX
PS Claim 18; Page 180; 299pp; English.
XX
CC The present invention describes an isolated polypeptide comprising an
CC immunogenic portion of an ovarian carcinoma protein (or its variants).
CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
CC cytostatic activity and can be used in gene therapy and vaccines. Ovarian
CC carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful
CC for the prevention, diagnosis and treatment of cancer, preferably ovarian
CC cancer. AA69691 to AA70077 and AB12552 to AB12557 represent human
CC ovarian carcinoma polynucleotides and proteins used in the
CC exemplification of the present invention
XX
SQ Sequence 184 BP, 61 A; 27 C; 47 G; 49 T; 0 U; 0 Other;
XX
Query Match 85.6%; Score 15.4; DB 3; Length 184;
Best Local Similarity 94.1%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CCGAAGGCGCTGTGCG 18
DB 112 CCGAAGGCGCTGTGCG 128
XX
RESULT 39
ABN72915
ID ABN72915 standard; DNA; 184 BP.
XX
AC ABN72915;
XX
DT 02-JUL-2002 (first entry)
XX
DE Ovarian carcinoma antigen polynucleotide #20.
XX
KM Human; immunostimulant; cytostatic; cancer; ovarian carcinoma; ds.
XX
OS Homo sapiens.
XX
PN WO200206317-A2.
XX
PD 24-JAN-2002.
XX
PF 17-JUL-2001; 2001WO-US022635.
XX
PR 17-JUL-2000; 2000US-00617747.
XX
PR 10-AUG-2000; 2000US-00636801.
XX
PR 20-SEP-2000; 2000US-00667857.
XX
PR 04-APR-2001; 2001US-00827271.
XX
PR 18-JUN-2001; 2001US-00884441.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
DR WPI; 2002-164781/21.
XX
PT Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer.
XX
PS Example 2; Page 298; 408pp; English.
XX
CC This invention relates to polypeptides comprising an immunogenic portion
CC of an ovarian carcinoma protein which acts as an immunostimulant and is
CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion

CC proteins, T cell populations and antigen presenting cells that express
CC the polypeptides are useful for stimulating an immune response in a
CC patient and treating ovarian cancer. This sequence represents DNA related
CC to the invention
XX
SQ Sequence 184 BP, 61 A; 27 C; 47 G; 49 T; 0 U; 0 Other;
XX
Query Match 85.6%; Score 15.4; DB 6; Length 184;
Best Local Similarity 94.1%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CCGAAGGCGCTGTGCG 18
DB 112 CCGAAGGCGCTGTGCG 128
XX
RESULT 40
ADA08485
ID ADA08485 standard; DNA; 184 BP.
XX
AC ADA08485;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human ovarian carcinoma antigen polynucleotide #330.
XX
KM ds; human; gene therapy; ovarian cancer; cancer.
XX
OS Homo sapiens.
XX
PN US2003091580-A1.
XX
PD 15-MAY-2003.
XX
PF 17-JUL-2001; 2001US-00907969.
XX
PR 18-JUN-2001; 2001US-00884441.
XX
PA (MITC/) MITCHAM J L.
PA (KING/) KING G E.
PA (ALGA/) ALGATE P A.
PA (FLIN/) FLING S P.
PA (RETT/) RETTER M W.
PA (FANG/) FANGER G R.
PA (REED/) REED S G.
PA (VEDV/) VEDVICK T S.
PA (CART/) CARTER D.
PA (HILL/) HILL P.
PA (ALBO/) ALBONE E.
XX
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR;
PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
XX
DR WPI; 2003-532352/50.
XX
PT New isolated O772P polypeptides and polynucleotides, useful in gene
PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian
PT cancer.
XX
PS Example 2; SEQ ID NO 332; 371pp; English.
XX
CC The invention relates to an isolated O772P polypeptide, which has the
CC structure fully defined in the specification. The composition containing
CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
CC or antigen presenting cells are useful for stimulating an immune response
CC and treating ovarian cancer. Detecting the presence of the
CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
CC carcinoma cDNAs and protein cDNAs were identified using microarray
CC technology. The present sequence represents a human ovarian carcinoma
CC antigen polynucleotide.
XX
SQ Sequence 184 BP, 61 A; 27 C; 47 G; 49 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 8; Length 184;
Best Local Similarity 94.1%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
2 CCGGAGGCGAGTCTGGC 18
112 CCAGAGGCGAGTCTGGC 128

RESULT 41
AA129201/c
ID AA129201 standard; cDNA; 405 BP.

AA129201;

12-OCT-2001 (first entry)

Colon tumour related determined cDNA sequence for clone R0093:H07.

Human; immunotherapy; diagnosis; colon cancer; colon tumour; immunogenic;
gene therapy; vaccine; colonic cancer; ss.

Homo sapiens.

WC200149716-A2.

12-JUL-2001.

29-DEC-2000; 2000WC-US035596.

30-DEC-1999; 99US-00476296.

10-JAN-2000; 2000US-00480321.

15-FEB-2000; 2000US-00504629.

06-MAR-2000; 2000US-00519444.

19-MAY-2000; 2000US-00575251.

29-JUN-2000; 2000US-00609448.

28-AUG-2000; 2000US-00649811.

(CORI-) CORIXA CORP.

Colo. tumor associated proteins and nucleic acids useful for the

prevention, diagnosis and treatment of colonic cancer.

Claim 2; Page 347; 472pp; English.

The present invention describes colon tumour associated proteins (I) and the polynucleotides (II) that encode them. (I) have cytoskeletal activity. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate colon tumour associated protein (TCAP) expression, such as colonic cancer. For example, (I) and (II) may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of TCAPs by expressing inactive proteins or to supplement the patients own production of them. Additionally, (II) may be used to produce the TCAP proteins by inserting the nucleic acids into a host cell culturing the cell to express the protein. (II) and its complementary sequences may also be used as DNA probes in diagnostic polymerase chain reaction (PCR) and hybridisation assays to detect and quantitate the presence of similar nucleic acids in samples, and therefore which patients may be in need of restorative therapy. (I) may also be used as antigens in the production of antibodies against TCAPs and in assays to identify modulators of TCAP expression and activity. Anti-(I) antibodies and antagonists may also be used to down regulate TCAP expression and activity. The anti-(I) antibodies may also be used as diagnostic agents for detecting the presence of TCAPs in samples (e.g. by enzyme linked immunosorbent assay (ELISA)). AA128460 to AA129512 and AA244494 to AA24523 represent nucleotide and amino acid sequences given in the exemplification of the

CC present invention
XX Sequence 405 BP; 106 A; 100 C; 77 G; 117 T; 0 U; 5 Other;
SQ
Query Match 85.6%; Score 15.4; DB 4; Length 405;
Best Local Similarity 94.1%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
2 CCGGAGGCGAGTCTGGC 18
213 CCAGAGGCGAGTCTGGC 197

RESULT 42
AB233387/c
ID AB233387 standard; cDNA; 405 BP.

AB233387;

30-JAN-2003 (first entry)

Human colon tumour cDNA for clone R0093:H07 SEQ ID NO: 755.

Human; colon cancer; colon tumour; immunotherapy; diagnosis; cancer;
tumour; immune response; immunostimulant; cytostatic; vaccine; gene; ss.

Homo sapiens.

WC200283070-A2.

24-OCT-2002.

09-APR-2002; 2002WC-US011475.

10-APR-2001; 2001US-00833263.

03-AUG-2001; 2001US-00922217.

19-DEC-2001; 2001US-00025380.

(CORI-) CORIXA CORP.

Colo. tumor associated proteins and nucleic acids useful for the

prevention, diagnosis and treatment of colonic cancer.

Claim 2; Page 349; 537pp; English.

The present invention describes compounds (1) for the immunotherapy and diagnosis of colon cancer. Also described: (1) a method for detecting the presence of cancer in a patient; (2) a method for stimulating and/or expanding T cells specific for a tumour protein; (3) an isolated T cell population comprising T cells prepared by the method of (2); (4) a method for stimulating an immune response in a patient; (5) a method for treating cancer in a patient; and (6) a method for inhibiting the growth of cancer in a patient. (I) have immunostimulant and cytostatic activities and can be used in vaccines. AB233646 to AB233725 and ABP5343 to ABP5391 represent human colon cancer/tumour related sequences used in the exemplification of the present invention
SQ Sequence 405 BP; 106 A; 100 C; 77 G; 117 T; 0 U; 5 Other;
Query Match 85.6%; Score 15.4; DB 7; Length 405;
Best Local Similarity 94.1%; Pred. No. 5.1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
2 CCGGAGGCGAGTCTGGC 18
213 CCAGAGGCGAGTCTGGC 197

RESULT 43
ACD95349/c
ID ACD95349 standard; cDNA: 428 BP.
XX
AC ACD95349;
XX
DT 23-SEP-2003 (first entry)
XX
DE Human colon cancer cell expressed cDNA #3761.
XX
KM Open reading frame detection; genome sequencing; colon cancer;
KM breast cancer; population genome analysis; genetic shift; cancer;
KM antibiotic resistance; antibiotic non-tolerance; congenital disease;
KM agriculture; food crop genome; resistance gene; retrovirus;
KM influenza virus; eukaryotic pathogen detection; trypanosome; Plasmodium;
KM gene; ss.
XX
OS Homo sapiens.
XX
FN US2002155438-A1.
XX
PD 24-OCT-2002.
XX
PF 27-SEP-1999; 99US-00406117.
XX
PR 20-NOV-1998; 98US-00196716.
XX
PA (SIMP/) SIMPSON A J G.
PA (NETO/) NETO E D.
PA (BREN/) BRENTANI R R.
XX
PI Simpson AJG, Neto ED, Brentani RR;
XX
DR WPI; 2003-182626/18.
XX
PT Determining open reading frames of genome of an organism e.g. a human
PT suffering from cancer involves use of single oligonucleotide primer at
PT low stringency for preparing single-stranded cDNA from mRNA of
PT individual.
XX
PS Example 9; Page 548; 959pp; English.
XX
CC The invention describes a method of determining open reading frames in
CC the genome of organism, comprising contacting mRNA from cell of organism
CC with a single oligonucleotide primer (I) at low stringency, preparing
CC single-stranded cDNA by reverse transcribing mRNA with (II), amplifying
CC cDNA, sequencing the product, and repeating the contacting, preparing
CC and amplifying steps with different primers and sequencing, resulting
CC nucleic acids. The method is useful for: determining that a known
CC nucleotide sequence from a genome of an organism corresponds to a
CC nucleotide sequence of an open reading frame; for preparing a contig;
CC nucleic acid molecule from a genome of an organism; and for sequencing
CC all or part of a genome of an organism. mRNA is obtained from mammalian
CC or human cell which is associated with a pathological condition e.g. a
CC colon cancer or breast cancer cell. The method is useful for analyses of
CC populations of subjects and can be used to carry out genetic analyses of
CC large or small populations. Further, it can be used to study living
CC systems to determine if, e.g. there have been genetic shifts which render
CC an individual or population more or less likely to be afflicted with
CC diseases such as cancer, to determine antibiotic resistance or non-
CC tolerance, and so forth. The method can also be used in the study of
CC congenital diseases, and the risk of affliction to a foetus, as well as
CC the study of whether the conditions are likely to be passed to offspring
CC through ova or sperm. The analyses for pathological conditions can be
CC carried out in all animals, plants, birds, fish, etc. Using this method,
CC in the area of agriculture, for example the genomes of food crops can be
CC studied to determine if resistance genes are present, defects in plant
CC genomes can also be studied in this way. Similarly, the method permits
CC determination of the pathogens which integrate into the genome, such as
CC retroviruses and other integrating viruses such as influenza virus, have
CC undergone shifts or mutations, which may require different approaches to
CC therapy. This method is also applied to eukaryotic pathogens, such as

CC trypanosomes, different types of Plasmodium, etc. The method essentially
CC eliminates sequencing of non-coding portions. This sequence represents a
CC polynucleotide isolated from human colon cancer cell cDNA library
XX

SO Sequence 428 BP; 123 A; 101 C; 79 G; 125 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 7; Length 428;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGAGCTGCG 18
DB 33 CAGGAAGGAGCTGCG 17

RESULT 44
ID ABK39596/c
XX ABK39596 standard; cDNA: 447 BP.
XX
AC ABK39596;
XX
DT 21-MAY-2002 (first entry)
XX
DE cDNA encoding lung tumour protein clone R0129.G02.
XX
KM Lung tumour; cancer; T cell; immune response stimulator; cytostatic;
KM gene; ss.
XX
OS Homo sapiens.
XX
FN WO200204514-A2.
XX
PD 17-JAN-2002.
XX
PF 10-JUL-2001; 2001WO-US022058.
XX
PR 11-JUL-2000; 2000US-00614124.
XX
PR 29-AUG-2000; 2000US-00651563.
XX
PR 08-SEP-2000; 2000US-00658824.
XX
PR 26-SEP-2000; 2000US-00671325.
XX
PR 06-OCT-2000; 2000US-00677419.
XX
PR 30-OCT-2000; 2000US-00702705.
XX
PR 13-DEC-2000; 2000US-00736457.
XX
PR 03-MAY-2001; 2001US-00849626.
XX
PA (CORI-) CORIXA CORP.
XX
PI Wang T, Matanabe Y, Henderson RA, Johnson JC, Retter MW;
PI Marnerakis M, Carter D, Fanger GR, Vedavick TS, Bangur CS, McNabb A;
PI Wang A, Fanger N, Switzer A, McNeill PD, Clapper JD;
XX
DR WPI; 2002-164634/21.
XX
PT Novel polynucleotide encoding a lung tumor polypeptide useful for
PT stimulating and/or expanding T cells specific for a tumor protein.
XX
PS Claim 1; SEQ ID NO 1634; 223pp; English.
XX
CC The invention describes an isolated polynucleotide and polypeptide useful
CC for stimulating and/or expanding T cells specific for a tumor protein
CC for determining the presence of a cancer in a patient. A composition
CC containing the polynucleotide and/or polypeptide is useful for treating a
CC lung cancer in a patient. The polypeptide is useful for removing tumor
CC cells from a biological sample. The polynucleotide is also useful as
CC probe or primer to detect the level of mRNA encoding a tumor protein.
CC This sequence encodes a lung tumour associated protein or protein
CC fragment, described in the method of the invention. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic format directly from WIPO at
CC ftp://ipo.int/pub/published_pct_sequences
XX
SQ Sequence 447 BP; 129 A; 105 C; 80 G; 133 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 6; Length 447;
 Best Local Similarity 94.1%; Pred. No. 5.2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCGAGTCTGCG 18
 |||||
 DB 73 CCGAAGGCGAGTCTGCG 57

RESULT 45
 ACA11925/c
 ID ACA11925 standard; cDNA; 447 BP.
 AC ACA11925;
 DT 05-JUN-2003 (first entry)
 DE Human lung adenocarcinoma library; cDNA SEQ ID 1634.
 XX Human; lung cancer; ss; lung tumour; cytostatic; vaccine;
 KM T cell expansion; CD4; CD8.
 XX Homo sapiens.
 OS
 PN US2002197669-A1.
 XX 26-DEC-2002.
 PD
 XX 03-MAY-2001; 2001US-00849626.
 PF
 XX 13-DEC-2000; 2000US-00736457.
 PR
 XX (BANG/) BANGUR C S.
 PA (FANG/) FANGER G R.
 PA (WANG/) WANG A.
 PA (WANG/) WANG T.
 PA (SWIT/) SWITZER A P.
 PA (MCNE/) MCNEILL P D.
 PA (CLAP/) CLAPPER J D.
 XX
 PI Bangur CS, Fanger GR, Wang A, Wang T, Switzer AP, McNeill PD;
 PI Clapper JD;
 PI
 XX WPI; 2003-352750/33.
 DR
 XX Novel lung cancer polynucleotide encoding lung cancer protein, useful for
 PT detecting the presence of lung cancer in a patient, and in pharmaceutical
 PT compositions, e.g. vaccines, for treating lung cancer.
 XX
 XX Example 1; Page; 72pp; English.

The invention relates to a polynucleotide encoding a lung tumour protein,
 comprising a sequence selected from any of the 14 sequences mentioned in
 the specification, or a sequence (S2) mentioned in specification,
 complement of S1, sequences consisting of at least 20 contiguous residues
 of S1, sequences that hybridise to S1, sequences having 75%, preferably
 90%, identity to S1, or degenerate variants of S1. Also included are an
 isolated polypeptide (comprising a sequence (S3) selected from any one of
 the 4 amino acid sequences mentioned in the specification, a sequence
 encoded by the polynucleotide, or sequences having at least 70%,
 preferably 90%, identity to a sequence encoded by the polynucleotide), an
 expression vector comprising the polynucleotide operably linked to an
 expression control sequence, a host cell transformed or transfected with
 the vector, an isolated antibody (or its antigen-binding fragment) that
 specifically binds to the polypeptide, detecting the presence of a cancer
 in a patient, a fusion protein comprising the polypeptide, an
 oligonucleotide that hybridises to S1 under moderately stringent
 conditions, stimulating and/or expanding T cells specific for a tumour
 protein (comprising contacting T cells with the polynucleotide, protein
 or antigen-presenting cells, under conditions and for a time sufficient
 to permit the stimulating and/or expansion of T cells) and inhibiting the
 development of a cancer in a patient (by incubating CD4⁺ and/or CD8⁺ T
 cells isolated from a patient with the polynucleotide, protein or antigen

CC presenting cells that express the polynucleotide, such that T cells
 CC proliferate, administering to the patient an effective amount of the
 CC proliferated T cells, and thus inhibiting the development of a cancer in
 CC the patient. The polynucleotide, protein and cells are useful in a
 CC composition for stimulating an immune response in a patient, and for
 CC treating a cancer in a patient (particularly lung cancer). The
 CC oligonucleotide is useful for determining the presence of a cancer in a
 CC patient. The protein and oligonucleotides are useful in pharmaceutical
 CC compositions, e.g. vaccines. The polynucleotide is also useful as a probe
 CC or primer for nucleic acid hybridisation, and in the design and
 CC preparation of ribozyme molecules for inhibiting expression of tumour
 CC polypeptides and proteins in tumour cells. An amplified portion of the
 CC polynucleotide is useful for isolating a full-length gene from a suitable
 CC library. The present sequence is a cDNA (full length, extended or
 CC partial) isolated from a library derived from lung tumour/cancer cells.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from the
 CC USPTO at seqdata.uspto.gov/sequence.html?docId=20020197669

XX SQ Sequence 447 BP; 129 A; 105 C; 80 G; 133 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 7; Length 447;
 Best Local Similarity 94.1%; Pred. No. 5.2e+02;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCGAGTCTGCG 18
 |||||
 DB 73 CCGAAGGCGAGTCTGCG 57

RESULT 46
 ACA03111/c
 ID ACA03111 standard; cDNA; 447 BP.
 AC ACA03111;
 DT 22-MAY-2003 (first entry)
 DE Lung cancer therapy and diagnosis associated cDNA #1600.
 XX Lung cancer; cytostatic; vaccine; gene therapy; cancer; gene; ss.
 KM
 XX Homo sapiens.
 OS
 PN US2002172952-A1.
 XX 21-NOV-2002.
 PD
 XX 10-JUL-2001; 2001US-00902941.
 PF
 XX 30-JUN-1999; 99US-00346492.
 PR 15-OCT-1999; 99US-00419356.
 PR 17-DEC-1999; 99US-00466867.
 PR 30-DEC-1999; 99US-00476300.
 PR 06-MAR-2000; 2000US-00518642.
 PR 22-MAR-2000; 2000US-00535077.
 PR 10-APR-2000; 2000US-00546259.
 PR 27-APR-2000; 2000US-00560406.
 PR 05-JUN-2000; 2000US-00589184.
 PR 11-JUL-2000; 2000US-00614124.
 PR 29-AUG-2000; 2000US-00651563.
 PR 08-SEP-2000; 2000US-00688824.
 PR 26-SEP-2000; 2000US-00671325.
 PR 06-OCT-2000; 2000US-00677419.
 PR 30-OCT-2000; 2000US-00702705.
 PR 13-DEC-2000; 2000US-00736457.
 PR 03-MAY-2001; 2001US-00849626.
 XX
 XX (CORI-) CORIXA CORP.
 PA
 PI Henderson RA, Wang T, Watanabe Y, Johnson JC, Retter MW,
 PI Durham M, Carter D, Fanger GR, Vedvick TS, Bangur CS, McNabb A;

DR WPI; 2003-328427/31.
XX
XX New polynucleotide, useful for preparing a composition for treating or
PT inhibiting development of cancer, e.g. lung cancer.
PT
XX
XX Example 1; SEQ ID NO 1634; 82pp; English.
PS
XX The invention describes an isolated polynucleotide comprising one of 32
CC sequences, complement or degenerate variants of them. The polynucleotide
CC is useful for preparing a composition e.g. a vaccine or for gene therapy,
CC for treating or inhibiting development of cancer, e.g. lung cancer. This
CC sequence represents a polynucleotide associated with the compositions and
CC methods for the therapy and diagnosis of lung cancer
XX
SQ Sequence 447 BP; 129 A; 105 C; 80 G; 133 T; 0 U; 0 Other;
Query Match 85.6%; Score 15.4; DB 7; Length 447;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CCGAAGGCGACTCTGCG 18
Db 73 CCGAAGGCGACTCTGCG 57
RESULT 47
ACH26026/c
ID ACH26026 standard; CDNA; 476 BP.
XX
XX ACH26026;
AC
XX
XX 13-OCT-2003 (first entry)
DT
XX
XX Human adult ovary cDNA #4406.
DE
XX
XX Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KM genome mapping; biodiversity; genetic disorder.
XX
XX Homo sapiens.
OS
XX
XX US2003073623-A1.
EN
XX
XX 17-APR-2003.
PD
XX
XX 30-JUL-2001; 2001US-00918995.
PF
XX
XX 30-JUL-2001; 2001US-00918995.
PR
XX
XX (DRNA/) DRMANAC R T.
XX (LABA/) LABAT I.
XX (STAC/) STACHE-CRAIN B.
XX (DICK/) DICKSON M C.
XX (JONE/) JONES L W.
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LM;
PI WPI; 2003-615964/58.
DR
XX
XX New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 13238; 44pp; English.
PS
XX The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a included frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for
CC identifying expressed genes or for physical mapping of the human genome,
CC in forensics, in assessing biodiversity, or in identifying mutations

CC responsible for genetic disorders and other traits. The nucleotide
CC sequences are also useful as hybridisation probes, as oligomers for PCR,
CC for chromosome and gene mapping, in the recombinant production of
CC protein, or in generating antisense DNA or RNA. The purified polypeptide
CC is useful for generating antibodies specific for it. The present sequence
CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC for this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from USPTO at
CC seqdata.uspto.gov/sequence.html?docid=20030073623
XX
SQ Sequence 476 BP; 130 A; 116 C; 91 G; 135 T; 0 U; 4 Other;
Query Match 85.6%; Score 15.4; DB 8; Length 476;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CCGAAGGCGACTCTGCG 18
Db 258 CCGAAGGCGACTCTGCG 242
RESULT 48
AAA16201/c
ID AAA16201 standard; DNA; 633 BP.
XX
XX AAA16201;
AC
XX
XX 14-JUN-2000 (first entry)
DT
XX
XX Human colon cancer differentially expressed nucleotide sequence #206.
DE
XX
XX Colon cancer; detect; differential expression; human; treatment;
KM detect mutation; non-invasive diagnostic method; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200012702-A2.
EN
XX
XX 09-MAR-2000.
PD
XX
XX 30-AUG-1999; 99WO-US019424.
PF
XX
XX 31-AUG-1998; 98US-0098639P.
PR
XX
XX 27-JAN-1999; 99US-0117393P.
XX
XX (FARB) BAYER CORP.
PA
XX
XX Endege WO, Steinmann KE, Aistle JH, Burgess CC, Carroll E;
PI Catino TU, Dwyer P, Ford DM, Lewis ME, Molino GA, Monahan JE;
PI Schlegel R;
PI WPI; 2000-256641/22.
DR
XX
XX Novel nucleic acids and proteins for identifying therapeutic agents
PT useful for treating and diagnosing cancer, especially colon cancer.
PT
XX
XX Claim 16; Page 206; 345pp; English.
PS
XX
XX This sequence represents a human nucleotide sequence which is
CC differentially expressed in colon cancer cells compared to the expression
CC levels in normal cells. The nucleotide sequence can be used as a source
CC of primers and probes. The nucleotide sequence is useful for determining
CC the phenotype of a cell by detecting the differential expression of the
CC sequence relative to a normal cell. The probes derived from the sequence
CC can also be used to determine the phenotype of cells in a sample. Probes
CC and antibodies which hybridise to the nucleotide sequence can also be
CC used to determine the phenotype of a cell. The primers are useful for
CC detecting a mutation in a test nucleotide sequence and also for detecting
CC cancer, preferably colon cancer. Antibodies against the protein encoded
CC by the nucleotide sequence can also be used in a method to detect colon
CC cancer. The diagnostic method is non-invasive and accurate for diagnosing
CC colon cancer at an early stage
XX

SQ Sequence 633 BP; 188 A; 151 C; 120 G; 172 T; 0 U; 2 Other;
Query Match 85.6%; Score 15.4; DB 3; Length 633;
Best Local Similarity 94.1%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 CCGAGAGGCACTCTGGC 18
DB 426 CCAGAGGCACTCTGGC 410
RESULT 49
AAFI7596
ID AAF17596 standard; cDNA; 647 BP.
AC AAF17596;
XX 13-MAR-2001 (first entry)
XX Human breast cancer associated coding sequence #8.
DE Human breast cancer associated gene; vaccine; diagnosis; therapy; ss.
XX Human; breast cancer associated gene; vaccine; diagnosis; therapy; ss.
OS Homo sapiens.
XX WO200060076-A2.
XX 12-OCT-2000.
XX 15-FEB-2000; 2000WO-US005308.
XX 02-APR-1999; 99US-00285480.
PR 23-JUN-1999; 99US-00339338.
PR 02-SEP-1999; 99US-00389681.
PR 03-NOV-1999; 99US-00433826.
XX (CORI-) CORIXA CORP.
XX Yuqiu J, Dillon DC, Mitcham JL, Xu J, Harlocker SL;
PI WPI; 2001-122627/13.
XX An isolated polypeptide useful for the treatment and diagnosis of tumors
PR e.g. breast cancer comprises at least an immunogenic portion of a breast
PT tumor protein.
XX Claim 66; Page 110; 238pp; English.
XX The present invention provides the coding sequences and some protein
CC sequences of proteins associated with breast cancer in humans. These
CC sequences can be used in the diagnosis and treatment of cancers,
CC particularly breast tumours
XX Sequence 647 BP; 216 A; 112 C; 129 G; 189 T; 0 U; 1 Other;
OY Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 CCGAGAGGCACTCTGGC 18
DB 575 CCAGAGGCACTCTGGC 591
RESULT 50
AAS47026
ID AAS47026 standard; cDNA; 647 BP.
AC AAS47026;
XX 18-DEC-2001 (first entry)
XX Human breast cancer cDNA clone #8.
DE

XX Human; ss; breast cancer protein; tumour; cancer; cytostatic;
XX gene therapy.
XX Homo sapiens.
XX WO200179286-A2.
XX 25-OCT-2001.
XX 12-APR-2001; 2001WO-US012164.
XX 17-APR-2000; 2000US-00551621.
PR 08-JUN-2000; 2000US-00590751.
PR 22-JUN-2000; 2000US-00604287.
PR 20-JUL-2000; 2000US-00620405.
XX (CORI-) CORIXA CORP.
XX Jiang Y, Dillon DC, Mitcham JL, Xu J, Harlocker SL, Hepler WT;
PI WPI; 2001-611721/70.
XX Breast Tumor Proteins and nucleic acids useful for the prevention,
PT diagnosis and treatment of breast cancer.
XX Claim 37; Page 169; 297pp; English.
XX The invention relates to isolated breast tumour proteins and nucleic
CC acids that encode them, including immunogenic fragments of the proteins.
CC Also included are expression vectors expressing the proteins, transformed
CC cells and antibodies raised against the proteins or an antigen presenting
CC cell expressing the protein. The proteins and nucleic acids may be used
CC in the prevention, diagnosis and treatment of diseases associated with
CC inappropriate breast tumour protein expression, i.e. breast tumours and
CC breast cancer e.g. by gene therapy. The nucleic acids and their
CC complements may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The
CC proteins, nucleic acids and antibodies may be used in assays to identify
CC modulators (e.g. antagonists) of breast tumour protein expression and
CC activity. The antibodies and antagonists may also be used to down
CC regulate expression and activity. The antibodies may also be used as
CC diagnostic agents for detecting the presence of the proteins in samples
CC (e.g. by enzyme linked immunosorbent assay (ELISA)) and in other immuno-
CC purification diagnostic techniques. The present sequence is a cDNA from a
CC breast tumour cDNA library isolated by subtractive hybridisation against
CC a normal breast cDNA library
XX Sequence 647 BP; 216 A; 112 C; 129 G; 189 T; 0 U; 1 Other;
OY Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 2 CCGAGAGGCACTCTGGC 18
DB 575 CCAGAGGCACTCTGGC 591
Search completed: March 5, 2004, 00:08:07
Job time : 354 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 22:59:05 ; Search time 1556 Seconds
(without alignments)

501.398 Million cell updates/sec

Title: US-09-848-868-35

Perfect score: 18

Sequence: 1 cccggaagcagctctggc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 200 summaries

Database :

```

1:  gb_da:*
2:  gb_htg:*
3:  gb_in:*
4:  gb_cm:*
5:  gb_ov:*
6:  gb_pat:*
7:  gb_ph:*
8:  gb_pl:*
9:  gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rnd:*
36: em_htg_man:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgc_hum:*
40: em_htgc_mus:*
41: em_htgc_other:*

```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	18	6	AX398039	AX398039 Sequence
2	18	100.0	36	6	AX298040	AX298040 Sequence
3	18	100.0	102	6	122245	122245 Sequence 15
4	18	100.0	102	6	HMP5302	M13112 Homo sapien
5	18	100.0	133	6	AR060418	AR060418 Sequence
6	18	100.0	133	6	AR128976	AR128976 Sequence
7	18	100.0	133	6	122232	122232 Sequence 2
8	18	100.0	133	6	HMP53A02	M22882 Human phosp
9	18	100.0	140	6	A69972	A69972 Sequence 3
10	18	100.0	167	9	AF209128	AF209128 Homo sapi
11	18	100.0	167	9	AF209129	AF209129 Homo sapi
12	18	100.0	167	9	AF209130	AF209130 Homo sapi
13	18	100.0	167	9	AF209131	AF209131 Homo sapi
14	18	100.0	167	9	AF209132	AF209132 Homo sapi
15	18	100.0	167	9	AF209133	AF209133 Homo sapi
16	18	100.0	167	9	AF209134	AF209134 Homo sapi
17	18	100.0	167	9	AF209135	AF209135 Homo sapi
18	18	100.0	167	9	AF209136	AF209136 Homo sapi
19	18	100.0	167	9	AF210308S1	AF210308 Homo sapi
20	18	100.0	255	6	A40037	A40037 Sequence 5
21	18	100.0	255	6	A69974	A69974 Sequence 5
22	18	100.0	800	6	192481	192481 Sequence 1
23	18	100.0	1303	6	122243	122243 Sequence 13
24	18	100.0	1303	6	AX006172	AX006172 Sequence
25	18	100.0	1303	6	BD073938	BD073938 Assay, re
26	18	100.0	1303	6	HMT253B	M14695 Human p53 c
27	18	100.0	1307	6	122242	122242 Sequence 12
28	18	100.0	1307	9	HMT253A	M14694 Human p53 c
29	18	100.0	1317	6	A67149	A67149 Sequence 6
30	18	100.0	1317	6	AR064393	AR064393 Sequence
31	18	100.0	1317	6	AR123180	AR123180 Sequence
32	18	100.0	1317	6	AR157699	AR157699 Sequence
33	18	100.0	1317	6	128707	128707 Sequence 1
34	18	100.0	1317	6	189361	189361 Sequence 1
35	18	100.0	1317	6	AR181303	AR181303 Sequence
36	18	100.0	1317	6	AR218593	AR218593 Sequence
37	18	100.0	1317	6	AX057140	AX057140 Sequence
38	18	100.0	1317	6	AX203243	AX203243 Sequence
39	18	100.0	1317	6	BD064183	BD064183 Methods fo
40	18	100.0	1317	9	HSP53	X02469 Human mRNA
41	18	100.0	1760	6	E13558	E13558 Mutated p53
42	18	100.0	1760	6	E13737	E13737 cDNA encodi
43	18	100.0	1760	6	BD084820	BD084820 Diagnos
44	18	100.0	1760	6	HMP53T	K03199 Human p53 c
45	18	100.0	2355	12	AF192534	AF192534 Expressi
46	18	100.0	2451	9	AB082923	AB082923 Homo sapi
47	18	100.0	2508	9	BC003596	BC003596 Homo sapi
48	18	100.0	2521	9	AF307851	AF307851 Homo sapi
49	18	100.0	3407	9	HOMOTSP1	AF135120 Homo sapi
50	18	100.0	3423	9	HSW059JPI	X54156 Human p53 g
51	18	100.0	20303	9	HSP53G	U94788 Human p53 (
52	18	100.0	20303	9	HSU94788	AC087388 Homo sapi
53	18	100.0	121017	9	AC087388	AC129971 Pan trogl
54	18	100.0	163542	2	AC129971	AC008049 Homo sapi
55	18	100.0	166941	2	AC008049	AC127470 Pan trogl
56	18	100.0	218485	2	AC127470	106689 Sequence 2
57	17	94.4	28	6	AC118242	AC118242 Mus muscu
58	17	94.4	68749	2	AL592215	AL592215 Mouse DNA
59	17	94.4	219468	10	AC023364	AC023364 Mus muscu
60	17	94.4	219720	1	AC023364	BRX21859 Xistrom
61	17	94.4	316050	5	AR360397	AR360397 Xenopus 1
62	16.4	91.1	577	5	AX202072	AX202072 Sequence
63	16.4	91.1	1986	6	MACP53A	L20442 Rhesus monk
64	16.4	91.1	1986	6	MACP53A	L20442 Rhesus monk
65	16.4	91.1	59257	9	AC106019	AC106019 Homo sapi

C 66	15.4	91.1	65545	2	AC139371	Homo sapi	C 139	15.4	85.6	11452	1	AE006030	Caulobact
C 67	16.4	91.1	70946	9	AL161614	Human DNA	C 140	15.4	85.6	13427	1	AE015175	AE015175 Shigella
C 68	16.4	91.1	121826	9	AL354935	Human DNA	C 141	15.4	85.6	13823	1	D90812	D90812 E.coli geno
C 69	16.4	91.1	158892	2	AC132819	Homo sapi	C 142	15.4	85.6	28798	9	HSA011107	Y11107 Homo sapien
C 70	16.4	91.1	164282	2	AC015733	Homo sapi	C 143	15.4	85.6	34642	9	AC003965	AC003965 Homo sapi
C 71	16.4	91.1	166525	2	AC022413	Homo sapi	C 144	15.4	85.6	41721	9	AC145291	AC145291 Homo sapi
C 72	16.4	91.1	170212	9	AC058822	Homo sapi	C 145	15.4	85.6	49736	1	AF319998	AF319998 Stigmarel
C 73	16.4	91.1	174521	2	AC127468	Papio anu	C 146	15.4	85.6	52603	9	AC016985	AC016985 Homo sapi
C 74	16.4	91.1	176927	2	AC127469	Papio anu	C 147	15.4	85.6	52666	9	AC003030	AC003030 Homo sapi
C 75	16.4	91.1	196037	9	AC129492	Homo sapi	C 148	15.4	85.6	63544	2	AC145792	AC145792 Silurana
C 76	16.4	91.1	196838	2	AC151596	Rattus no	C 149	15.4	85.6	67016	9	AC008767	AC008767 Homo sapi
C 77	16.4	91.1	196840	2	AC023255	Rattus no	C 150	15.4	85.6	76665	4	AC091723	AC091723 Sus scrof
C 78	16.4	91.1	231746	2	AC013389	Homo sapi	C 151	15.4	85.6	77489	2	AC139552	AC139552 Homo sapi
C 79	16.4	91.1	231109	2	AC011864	Homo sapi	C 152	15.4	85.6	78419	3	AC004639	AC004639 Homo sapi
C 80	16.4	91.1	233308	2	AC112290	Rattus no	C 153	15.4	85.6	81786	9	AC003002	AC003002 Homo sapi
C 81	16.4	91.1	233678	2	AC110557	Rattus no	C 154	15.4	85.6	82019	2	AC139567	AC139567 Homo sapi
C 82	16.4	91.1	257092	2	AC097308	Rattus no	C 155	15.4	85.6	89885	3	AC004368	AC004368 Drosophill
C 83	16.4	91.1	282895	2	AC096056	Rattus no	C 156	15.4	85.6	91099	9	AC110280	AC110280 Homo sapi
C 84	16.4	91.1	282895	2	AC096056	Rattus no	C 157	15.4	85.6	93634	2	AC127088	AC127088 Homo sapi
C 85	16.4	91.1	144885	10	AL7731766	Mouse DNA	C 158	15.4	85.6	105692	2	AP003953	AP003953 Oryza sat
C 86	16.4	91.1	187081	10	AL7731766	Mouse DNA	C 159	15.4	85.6	110000	9	HSR63451	HSR63451 Continuation (2 of
C 87	16.4	91.1	214284	9	AC116643	Homo sapi	C 160	15.4	85.6	111293	9	AC000377	AC000377 Homo sapi
C 88	16.4	91.1	227769	2	AC112437	Rattus no	C 161	15.4	85.6	116215	9	AC004130	AC004130 Homo sapi
C 89	16.4	91.1	246913	2	AC113620	Rattus no	C 162	15.4	85.6	118873	9	HS118494	HS118494 Homo sapi
C 90	16.4	91.1	254175	2	AC096015	Rattus no	C 163	15.4	85.6	120831	4	AC137644	AC137644 Artibeus
C 91	16.4	91.1	254175	2	AC096015	Rattus no	C 164	15.4	85.6	122948	9	HSR91821	HSR91821 Homo sapi
C 92	16.4	91.1	184	6	AR264946	Sequence	C 165	15.4	85.6	127361	9	AC007283	AC007283 Homo sapi
C 93	16.4	91.1	184	6	AR264946	Sequence	C 166	15.4	85.6	127361	2	AC147500	AC147500 Mus muscu
C 94	16.4	91.1	184	6	AR264946	Sequence	C 167	15.4	85.6	129630	2	AC002403	AC002403 Homo sapi
C 95	16.4	91.1	370	4	AY055474	Myotis lu	C 168	15.4	85.6	132963	2	AC017518	AC017518 Drosophill
C 96	16.4	91.1	405	6	AX193188	Sequence	C 169	15.4	85.6	133815	9	AC124055	AC124055 Homo sapi
C 97	16.4	91.1	447	6	AR273891	Sequence	C 170	15.4	85.6	137271	2	AC102823	AC102823 Mus muscu
C 98	16.4	91.1	447	6	AR273891	Sequence	C 171	15.4	85.6	138347	9	AL389889	AL389889 Human DNA
C 99	16.4	91.1	447	6	AR273891	Sequence	C 172	15.4	85.6	144741	8	AP004674	AP004674 Oryza sat
C 100	16.4	91.1	447	6	AR273891	Sequence	C 173	15.4	85.6	148055	9	AC026414	AC026414 Homo sapi
C 101	16.4	91.1	447	10	RNO131888	Rattus no	C 174	15.4	85.6	148356	2	AC144886	AC144886 Bos tauru
C 102	16.4	91.1	633	6	BD229531	Human gen	C 175	15.4	85.6	153937	2	AC023953	AC023953 Homo sapi
C 103	16.4	91.1	633	6	AF134585	Callithrix	C 176	15.4	85.6	156135	9	AC093799	AC093799 Homo sapi
C 104	16.4	91.1	647	6	AR280576	Sequence	C 177	15.4	85.6	156683	9	AC091891	AC091891 Homo sapi
C 105	16.4	91.1	647	6	AR280576	Sequence	C 178	15.4	85.6	157259	2	AC016976	AC016976 Homo sapi
C 106	16.4	91.1	647	6	AR280576	Sequence	C 179	15.4	85.6	158043	9	AC105270	AC105270 Homo sapi
C 107	16.4	91.1	647	6	AR280576	Sequence	C 180	15.4	85.6	158310	10	AL162571	AL162571 Homo sapi
C 108	16.4	91.1	647	6	AR280576	Sequence	C 181	15.4	85.6	159056	10	ALR64368	ALR64368 Mouse DNA
C 109	16.4	91.1	647	6	AR280576	Sequence	C 182	15.4	85.6	162686	8	ATR06156	ATR06156 Amborella
C 110	16.4	91.1	647	6	AR280576	Sequence	C 183	15.4	85.6	163417	9	AC005043	AC005043 Homo sapi
C 111	16.4	91.1	647	6	AR280576	Sequence	C 184	15.4	85.6	163954	2	AC017155	AC017155 Drosophill
C 112	16.4	91.1	952	1	AY349571	Unculture	C 185	15.4	85.6	165857	9	AP006463	AP006463 Homo sapi
C 113	16.4	91.1	1017	1	PR0065707	Unculture	C 186	15.4	85.6	167254	2	AC146109	AC146109 Pan trogl
C 114	16.4	91.1	1017	12	BT008006	Synthetic	C 187	15.4	85.6	168652	9	AC022024	AC022024 Homo sapi
C 115	16.4	91.1	1066	1	BSPP313427	Brevundim	C 188	15.4	85.6	169873	2	AC079881	AC079881 Homo sapi
C 116	16.4	91.1	1066	1	AX014102	Sequence	C 189	15.4	85.6	170595	2	AC025957	AC025957 Homo sapi
C 117	16.4	91.1	1548	6	BD204672	Human nuc	C 190	15.4	85.6	172574	2	AC011121	AC011121 Homo sapi
C 118	16.4	91.1	1548	6	BD204672	Human nuc	C 191	15.4	85.6	173055	2	AC118579	AC118579 Didelphis
C 119	16.4	91.1	1548	6	AX336369	Sequence	C 192	15.4	85.6	173081	3	AC110170	AC110170 Mus muscu
C 120	16.4	91.1	1548	6	AX336369	Sequence	C 193	15.4	85.6	173273	10	AC009351	AC009351 Drosophill
C 121	16.4	91.1	1548	6	AX336369	Sequence	C 194	15.4	85.6	173846	10	AL929065	AL929065 Mouse DNA
C 122	16.4	91.1	1548	6	AX336369	Sequence	C 195	15.4	85.6	173932	2	AC102837	AC102837 Mus muscu
C 123	16.4	91.1	1548	6	AX336369	Sequence	C 196	15.4	85.6	175610	9	AC073176	AC073176 Homo sapi
C 124	16.4	91.1	1548	6	AX336369	Sequence	C 197	15.4	85.6	175909	2	AC093559	AC093559 Homo sapi
C 125	16.4	91.1	1548	6	AX336369	Sequence	C 198	15.4	85.6	178515	9	AC015551	AC015551 Homo sapi
C 126	16.4	91.1	1548	6	AX336369	Sequence	C 199	15.4	85.6	179216	2	AC074016	AC074016 Homo sapi
C 127	16.4	91.1	1548	6	AX336369	Sequence	C 200	15.4	85.6	179848	2	AC139880	AC139880 Lemur cat
C 128	16.4	91.1	1548	6	AX336369	Sequence							
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C 130	16.4	91.1	1548	6	AX336369	Sequence							
C 131	16.4	91.1	1548	6	AX336369	Sequence							
C 132	16.4	91.1	1548	6	AX336369	Sequence							
C 133	16.4	91.1	1548	6	AX336369	Sequence							
C 134	16.4	91.1	1548	6	AX336369	Sequence							
C 135	16.4	91.1	1548	6	AX336369	Sequence							
C 136	16.4	91.1	1548	6	AX336369	Sequence							
C 137	16.4	91.1	1548	6	AX336369	Sequence							
C 138	16.4	91.1	1548	6	AX336369	Sequence							

ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

ACCESSION

VERSION

18 bp

DNA

linear PAT 26-NOV-2001

Sequence 35 from Patent WO0183740.

AX298039.1 GI:17128125

KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE
1
AUTHORS
Iversen, P.L. and Hudziak, R.
TITLE
Splice-region antisense composition and method
JOURNAL
Patent: WO 0183740-A 35 08-NOV-2001;
Avi Biopharma, Inc. (US)
LOCATION/Qualifiers

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/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="antisense"

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Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db
1 CCCGGAAGGCGAGTCTGGC 18
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1 CCCGGAAGGCGAGTCTGGC 18

RESULT 2
AX298040
LOCUS
AX298040
DEFINITION
Sequence 36 from Patent WO0183740.
ACCESSION
AX298040
VERSION
AX298040.1 GI:17128126
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.

REFERENCE
1
AUTHORS
Iversen, P.L. and Hudziak, R.
TITLE
Splice-region antisense composition and method
JOURNAL
Patent: WO 0183740-A 36 08-NOV-2001;
Avi Biopharma, Inc. (US)
LOCATION/Qualifiers

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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="antisense"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 36;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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17 CCCGGAAGGCGAGTCTGGC 34
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Db
17 CCCGGAAGGCGAGTCTGGC 34
|||||

RESULT 3
122245/c
LOCUS
122245
DEFINITION
Sequence 15 from patent US 5527676.
ACCESSION
122245
VERSION
122245.1 GI:1602599
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 102)
REFERENCE
Vogelstein, B., Baker, S.J., Pearson, R.R. and Nigro, J.M.
AUTHORS
TITLE
Detection of loss of the wild-type p53 gene and kites therefor
JOURNAL
Patent: US 5527676-A 15 18-JUN-1996;
LOCATION/Qualifiers

source
1..102
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 102;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 CCCGGAAGGCGAGTCTGGC 18
|||||
20 CCCGGAAGGCGAGTCTGGC 3
|||||

Db
20 CCCGGAAGGCGAGTCTGGC 3
|||||

RESULT 4
HUMP5302/c
LOCUS
HUMP5302
DEFINITION
Homo sapiens phosphoprotein p53 (TP53) gene, exon 2.
ACCESSION
M3112.1
VERSION
M3112.1 GI:189451
KEYWORDS
antigen; phosphoprotein; tumor antigen.
SEGMENT
2 of 11
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
AUTHORS
Lamb, P. and Crawford, L.
TITLE
Characterization of the human p53 gene
JOURNAL
Mol. Cell. Biol. 6 (5), 1379-1385 (1986)
MEDLINE
87064416
PUBMED
2946935
LOCATION/Qualifiers

FEATURES
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1..102
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/map="17p13.1"
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/gene="TP53"
/note="G00-120-445"
/number=2

ORIGIN
exon
Query Match 100.0%; Score 18; DB 9; Length 102;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1 CCCGGAAGGCGAGTCTGGC 18
|||||
20 CCCGGAAGGCGAGTCTGGC 3
|||||

Db
20 CCCGGAAGGCGAGTCTGGC 3
|||||

RESULT 5
AR060418/c
LOCUS
AR060418
DEFINITION
Sequence 22 from patent US 5840579.
ACCESSION
AR060418
VERSION
AR060418.1 GI:5986868
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
1 (bases 1 to 133)
REFERENCE
Boeke, J.D. and Brachmann, R.K.
AUTHORS
TITLE
Nucleic acids encoding p53 mutations which suppress p53 cancer
mutations
JOURNAL
Patent: US 5840579-A 22 24-NOV-1998;
LOCATION/Qualifiers

FEATURES
source
1..133
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 133;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCACTCTGGC 18
 DB 35 CCCGGAAGGCACTCTGGC 18

RESULT 6

LOCUS

ARI28976/c 133 bp DNA linear PAT 16-MAY-2001

DEFINITION Sequence 22 from patent US 6183964.

ACCESSION ARI28976

VERSION ARI28976.1 GI:14116638

KEYWORDS

SOURCE

ORGANISM

Unknown.

REFERENCE 1 (bases 1 to 133)

AUTHORS Boeke, U.D. and Brachmann, R.K.

TITLE Method for identifying suppressor mutations for common p53 cancer mutations

JOURNAL Patent: US 6183964-A 22 06-FEB-2001;

FEATURES

source

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/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

1 CCCGGAAGGCACTCTGGC 18

35 CCCGGAAGGCACTCTGGC 18

RESULT 7
 LOCUS 122232/c 133 bp DNA linear PAT 07-OCT-1996

DEFINITION Sequence 2 from patent US 5527676.

ACCESSION 122232

VERSION 122232.1 GI:1602586

KEYWORDS

SOURCE

ORGANISM

Unknown.

REFERENCE 1 (bases 1 to 133)

AUTHORS Vogelstein, B., Baker, S.C., Fearon, E.R. and Nigro, J.M.

TITLE Detection of loss of the wild-type p53 gene and kits therefor

JOURNAL Patent: US 5527676-A 2 18-JUN-1996;

FEATURES

source

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/organism="unknown"

/mol_type="unassigned DNA"

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

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35 CCCGGAAGGCACTCTGGC 18

100.0%; Score 18; DB 6; Length 133;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 LOCUS HUMF53A02/c 133 bp DNA linear PRI 08-JAN-1995

DEFINITION Human phosphoprotein p53 gene, exon 2.

ACCESSION M22882
 VERSION M22882.1 GI:169465
 KEYWORDS phosphoprotein p53.
 SEGMENT 2 of 11
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE 1 (bases 1 to 133)

AUTHORS Buchman, V.L., Chumakov, P.M., Ninkina, N.N., Samartina, O.P. and Georgiev, G.P.

TITLE A variation in the structure of the protein-coding region of the

JOURNAL human p53 gene

MEDLINE Gene 70 (2), 245-252 (1988)

COMMENT 2905688

FEATURES

Original source text: Homo sapiens placenta DNA.

source

1.133

/organism="Homo sapiens"

/mol_type="genomic DNA"

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/tissue_type="placenta"

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/number=1

/number=1

/gene="p53"

/product="phosphoprotein p53"

/number=2

ORIGIN

About 10400 bp after segment 1.

Query Match

Best Local Similarity

Matches

QY

DB

1 CCCGGAAGGCACTCTGGC 18

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RESULT 9
 LOCUS A69972 140 bp DNA linear PAT 07-MAY-1999

DEFINITION Sequence 3 from Patent WO9807851.

ACCESSION A69972

VERSION A69972.1 GI:4774443

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

Homo sapiens

REFERENCE 1 (bases 1 to 140)

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

TITLE AGENTS FOR THE PRE-SYMPTOMATIC DETECTION, PREVENTION AND TREATMENT

JOURNAL OF BREAST CANCER IN HUMANS

Patent: WO 9807851-A 3 26-FEB-1998;

FEATURES

source

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/clone="BC532L"

ORIGIN

Query Match

Best Local Similarity

Matches

QY

DB

1 CCCGGAAGGCACTCTGGC 18

14 CCCGGAAGGCACTCTGGC 31

100.0%; Score 18; DB 6; Length 140;
 Best Local Similarity 100.0%; Pred. No. 7.2e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
AF209128/c
LOCUS AF209128 167 bp DNA linear PRI 27-MAR-2003
DEFINITION Homo sapiens tumor suppressor p53 (TP53) gene, partial cds.
ACCESSION AF209128
VERSION AF209128.1 GI:7107284
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Thompson-Henir,J., Davies,M.P., Green,J.A., Halliwell,N., Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
TITLE Novel polymerase chain reaction approach for full-coding p53 mutation detection in microdissected archival tumors
JOURNAL Diagn. Mol. Pathol. 9 (2), 110-119 (2000)
MEDLINE 20306720
PUBMED 10850547
REFERENCE 2 (bases 1 to 167)
AUTHORS Thompson-Henir,J., Davies,M.P.A., Green,J.A., Halliwell,N., Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
TITLE Direct Submission
JOURNAL Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories, Clatterbridge Cancer Research Trust, Clatterbridge Hospital, Bebington, Wirral CH63 4UY, United Kingdom
LOCATION/Qualifiers
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source
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1. .>167
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exon
1. .21
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number=2
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db_xref="GI:7107285"
translation="MEBPQSDPSVPEPLSQETPSDLMLK"
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124. .>167
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number=2
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replace="cc"
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Query Match 100.0%; Score 18; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 CCCGAGGAGGAGCTGTGGC 18
|||||
Db 41 CCCGAGGAGGAGCTGTGGC 24
RESULT 11
AF209129/c
LOCUS AF209129 167 bp DNA linear PRI 27-MAR-2003

DEFINITION Homo sapiens tumor suppressor p53 (TP53) gene, partial cds.
ACCESSION AF209129
VERSION AF209129.1 GI:7107286
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
AUTHORS Thompson-Henir,J., Davies,M.P., Green,J.A., Halliwell,N., Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
TITLE Novel polymerase chain reaction approach for full-coding p53 mutation detection in microdissected archival tumors
JOURNAL Diagn. Mol. Pathol. 9 (2), 110-119 (2000)
MEDLINE 20306720
PUBMED 10850547
REFERENCE 2 (bases 1 to 167)
AUTHORS Thompson-Henir,J., Davies,M.P.A., Green,J.A., Halliwell,N., Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
TITLE Direct Submission
JOURNAL Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories, Clatterbridge Cancer Research Trust, Clatterbridge Hospital, Bebington, Wirral CH63 4UY, United Kingdom
LOCATION/Qualifiers
FEATURES
source
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db_xref="GI:7107287"
translation="MEBPQSDPSVPEPLSQETPSDLMLK"
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Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 CCCGAGGAGGAGCTGTGGC 18
|||||
Db 41 CCCGAGGAGGAGCTGTGGC 24
RESULT 12
AF209130/c
LOCUS AF209130 167 bp DNA linear PRI 27-MAR-2003
DEFINITION Homo sapiens tumor suppressor p53 (TP53) gene, partial cds.
ACCESSION AF209130
VERSION AF209130.1 GI:7107288
KEYWORDS
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Thompson-Hehir,J., Davies,M.P., Green,J.A., Halliwell,N.,
1 (bases 1 to 167)
TITLE Novel polymerase chain reaction approach for full-coding p53
mutation detection in microdissected archival tumors
JOURNAL Diagn. Mol. Pathol. 9 (2), 110-119 (2000)
MEDLINE 20306720
PUBMED 10850547
REFERENCE
AUTHORS 2 (bases 1 to 167)
Thompson-Hehir,J., Davies,M.P.A., Green,J.A., Halliwell,N.,
Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
DIRECT SUBMISSION
TITLE Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories,
Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
Bebington, Wirral CH63 4UY, United Kingdom
JOURNAL Location/Qualifiers
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100.0%; Score 18; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
Query Match 100.0%; Score 18; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 6.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 41 CCGGAGGCGAGTCTGGC 24

RESULT 13
AF209131/c 167 bp DNA linear PRI 27-MAR-2003
LOCUS Homo sapiens tumor suppressor p53 (TP53) gene, partial cds.
DEFINITION AF209131
ACCESSION AF209131.1 GI:7107290
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Thompson-Hehir,J., Davies,M.P., Green,J.A., Halliwell,N.,
1 (bases 1 to 167)
TITLE Novel polymerase chain reaction approach for full-coding p53
mutation detection in microdissected archival tumors
JOURNAL Diagn. Mol. Pathol. 9 (2), 110-119 (2000)
MEDLINE 20306720
PUBMED 10850547
REFERENCE
AUTHORS 2 (bases 1 to 167)
Thompson-Hehir,J., Davies,M.P.A., Green,J.A., Halliwell,N.,
Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
DIRECT SUBMISSION
TITLE Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories,
Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
Bebington, Wirral CH63 4UY, United Kingdom
JOURNAL Location/Qualifiers
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source 1..167
/organism="Homo sapiens"
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/chromosome="17"
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/tissue_type="head and neck carcinomas and associated
normal tissue"
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variation
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QY 1 CCGGAGGCGAGTCTGGC 18
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Db 41 CCGGAGGCGAGTCTGGC 24

RESULT 14
AF209132/c 167 bp DNA linear PRI 27-MAR-2003
LOCUS Homo sapiens cell-line Molt4 tumor suppressor p53 (TP53) gene,
partial cds.
DEFINITION AF209132
ACCESSION AF209132
VERSION AF209132.1 GI:7107292
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Thompson-Hehir,J., Davies,M.P., Green,J.A., Halliwell,N.,
1 (bases 1 to 167)
TITLE Novel polymerase chain reaction approach for full-coding p53
mutation detection in microdissected archival tumors
JOURNAL Diagn. Mol. Pathol. 9 (2), 110-119 (2000)
MEDLINE 20306720

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TITLE Novel polymerase chain reaction approach for full-coding p53
mutation detection in microdissected archival tumors
JOURNAL Diagn. Mol. Pathol. 9 (2), 110-119 (2000)
MEDLINE 20306720
PUBMED 10850547
REFERENCE
AUTHORS Thompson-Hehir,J., Davies,M.P.A., Green,J.A., Halliwell,N.,
Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.
DIRECT SUBMISSION
TITLE Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories,
Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
Bebington, Wirral CH63 4UY, United Kingdom
JOURNAL Location/Qualifiers
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
|||||
Db 41 CCGGAGGCGAGTCTGGC 24

RESULT 14
AF209132/c 167 bp DNA linear PRI 27-MAR-2003
LOCUS Homo sapiens cell-line Molt4 tumor suppressor p53 (TP53) gene,
partial cds.
DEFINITION AF209132
ACCESSION AF209132
VERSION AF209132.1 GI:7107292
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Thompson-Hehir,J., Davies,M.P., Green,J.A., Halliwell,N.,
1 (bases 1 to 167)
TITLE Novel polymerase chain reaction approach for full-coding p53
mutation detection in microdissected archival tumors
JOURNAL Diagn. Mol. Pathol. 9 (2), 110-119 (2000)
MEDLINE 20306720

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PUBLISHED		10850547
REFERENCE	J.	(bases 1 to 167)
AUTHORS	Thompson-Hehir,J., Davies,M.P.A., Green,J.A., Halliwell,N., Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.	
TITLE	Direct Submission	
JOURNAL	Submitted (30-NOV-1999) J.K. Douglas Cancer Research Laboratories, Clatterbridge Cancer Research Trust, Clatterbridge Hospital, Beblington, Wirral CH63 4UY, United Kingdom	
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Db	41 CCCGGAAGCGACTTGGC 24	
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LOCUS		
DEFINITION	Homo sapiens cell-line A431 tumor suppressor p53 (TP53) gene,	
ACCESSION	partial cds. AF209133	
VERSION	AF209133.1 GI:7107294	
KEYWORDS	.	
SOURCE	Homo sapiens (human) Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo. 1 (bases 1 to 167) Thompson-Hehir,J., Davies,M.P., Green,J.A., Halliwell,N., Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C. Novel polymerase chain reaction approach for full-coding p53 mutation detection in microdissected archival tumors Diagn.Mol.Pathol. 9 (2), 110-119 (2000)	
TITLE	Journal MEDLINE	
JOURNAL	20306720	
PUBLISHED	10850547	
REFERENCE	J.	(bases 1 to 167)
AUTHORS	Thompson-Hehir,J., Davies,M.P.A., Green,J.A., Halliwell,N., Joyce,K.A., Salisbury,J., Sibson,D.R., Vergote,I. and Walker,C.	
TITLE	Direct Submission	

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JOURNAL      Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories,
              Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
              Bebbington, Wirral CH63 4UY, United Kingdom

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  QY
    1 CCCGGAAGCAGCTGGC 18
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  Db 41 CCCGGAAGCAGCTGGC 24

RESULT 16
AF209134      167 bp      DNA      linear      PRI 27-MAR-2003
AF209134/c   Homo sapiens cell-line HT29 tumor suppressor p53 (TP53) gene,
LOCUS        partial cds.
DEFINITION   AF209134.1 GI:7107296
ACCESSION    AF209134
VERSION      AF209134
KEYWORDS     Homo sapiens (human)
SOURCE       Homo sapiens
ORGANISM     Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 167)
Thompson-Henri, J., Davies, M.P., Green, J.A., Halliwell, N.,
Joyce, K.A., Salisbury, J., Sibson, D.R., Vergote, I., and Walker, C.
Novel polymerase chain reaction approach for full-coding p53
mutation detection in microdissected archival tumors
Diagn. Mol. Pathol. 9 (2), 110-119 (2000)
2 (bases 1 to 167)
Thompson-Henri, J., Davies, M.P.A., Green, J.A., Halliwell, N.,
Joyce, K.A., Salisbury, J., Sibson, D.R., Vergote, I., and Walker, C.
Direct Submission
Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories,
Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
Bebington, Wirral CH63 4UY, United Kingdom
Location/Qualifiers
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LOCUS	AF209135
DEFINITION	Homo sapiens cell-line HeLa tumor suppressor p53 (TP53) gene,
ACCESION	AF209135
VERSION	AF209135
KEYWORDS	partial cds.
SOURCE	AF209135.1 GI:7107289
ORGANISM	Homo sapiens (human)
	Homo sapiens

REFERENCE
AUTHORS
1 (bases 1 to 167)
Thompson, H. J., Davies, M. P., Green, J. A., Halliwell, N.,

TITLE	Novel polymerase chain reaction approach for full-coding p53 mutation detection in microdissected archival tumors
JOURNAL	Diagn. Mol. Pathol. 9 (2), 110-119 (2000)

REFERENCE 2 (bases 1 to 167)
AUTHORS Thompson-Henir, J., Davies, M. P. A., Green, J. A., Halliwell, N.,

JOURNAL Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories
Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
Bebington, Wirral CH63 4JY, United Kingdom

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DY 1 CCGGAAGGCAGTCTGGC 18
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Ddb 41 CCGGAAAGCAGTCTGGC 24

RESULT 18	AF209136/c	167 bp	DNA	linear	PRI 27-MAR-2003
LOCUS	AF209136				
DEFINITION	Homo sapiens cell-line HNS tumor suppressor p53 (TP53) gene, partial cds.				
ACCESSION	AF209136				
VERSION	AF209136.1	GI:7107300			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				

REFERENCE
AUTHORS
1 (bases 1 to 167)
Thompson-Hehr, J., Davies, M. P., Green, J. A., Halliwell, N.,

mutation detection in microdissected archival tumors
Diagn. Mol. Pathol. 9 (2), 110-119 (2000)

PUBMED 10850547
REFERENCE 2 (bases 1 to 167)
AUTHORS Thompson-Henry, J., Davies, M. P. A., Green, J. A., Halliwell, N.,

JOURNAL Submitted (30-NOV-1999) J. K. Douglas Cancer Research Laboratories
Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
Bebington, Wirral CH63 4UY, United Kingdom

FEATURES
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QY 1 CCCGAGGAGCAGTCTGCG 18
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41 CCCGAGGAGCAGTCTGCG 24

RESULT 19
AF210308S1 167 bp DNA linear PRI 12-APR-2000
LOCUS AF210308S1
DEFINITION Homo sapiens p53 tumor suppressor protein (TP53) gene, exon 2.
ACCESSION AF210308
VERSION AF210308.1 GI:7542419
KEYWORDS
SEGMENT
1 of 3
SOURCE
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 167)
Joyce, K.A., Salisbury, J., Sibson, D.R., Vergote, I. and Walker, C.
Thompson-Henir, U., Davies, M.P.A., Green, J.A., Halliwell, N.,
Mutation Detection Utilizing a Novel PCR Approach for Amplification
of the p53 Gene from Microdissected Tissue: Application to Archival
Tumor Samples
Unpublished
2 (bases 1 to 167)
Thompson-Henir, U., Davies, M.P.A., Green, J.A., Halliwell, N.,
Joyce, K.A., Salisbury, J., Sibson, D.R., Vergote, I. and Walker, C.
Direct Submission
Submitted (01-DEC-1999) J.K. Douglas Cancer Research Laboratories,
Clatterbridge Cancer Research Trust, Clatterbridge Hospital,
Bebington, Wirral CH63 4UY, UK
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QY 1 CCCGAGGAGCAGTCTGCG 18
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41 CCCGAGGAGCAGTCTGCG 24

RESULT 20
A40037 255 bp DNA linear PAT 05-MAR-1997
LOCUS A40037
DEFINITION Sequence 5 from Patent WO9421791.
ACCESSION A40037
VERSION A40037.1 GI:2296203
KEYWORDS
SOURCE
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 255)
Bergman, J.E. and Predlie, R.E.
AGENTS FOR THE PREVENTION AND TREATMENT OF BREAST CANCER
Patent: WO 9421791-A 5 29-SEP-1994;
BERGMANN JOHANNA EUGENIE (DE)
Location/Qualifiers
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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCAGTCTGCG 18
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RESULT 21
A69974 255 bp DNA linear PAT 07-MAY-1999
LOCUS A69974
DEFINITION Sequence 5 from Patent WO9807851.
ACCESSION A69974
VERSION A69974.1 GI:4774444
KEYWORDS
SOURCE
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 255)
Predlie, R. and Bergmann, J.E.
AGENTS FOR THE PRE-SYMPTOMATIC DETECTION, PREVENTION AND TREATMENT
OF BREAST CANCER IN HUMANS
Patent: WO 9807851-A 5 26-FEB-1998;
PREDLIE ENRIQUE R (CA)
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DB 14 CCCGAGAGCAGTCTGGC 31

RESULT 22
LOCUS 192481/c
DEFINITION Sequence 1 from patent US 5728526.
ACCESSION 192481
VERSION 192481.1 GI:3936951
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 800)
AUTHORS George, A.L. Jr., Bhattacharya, S.K. and Nazarenko, I.
TITLES Method for analyzing a nucleotide sequence
JOURNAL Patent: US 5728526-A 1 17-MAR-1998;
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QY 1 CCCGAGAGCAGTCTGGC 18
DB 108 CCCGAGAGCAGTCTGGC 91

RESULT 23
LOCUS 122243/c
DEFINITION Sequence 13 from patent US 5527676.
ACCESSION 122243
VERSION 122243.1 GI:1602597
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1303)
AUTHORS Vogelstein, B., Baker, S.J., Fearon, E.R. and Nigro, J.M.
TITLES Detection of loss of the wild-type P53 gene and kits therefor
JOURNAL Patent: US 5527676-A 13 18-JUN-1996;
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ORIGIN

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DB 113 CCCGAGAGCAGTCTGGC 96

RESULT 24
LOCUS AX006172/c
DEFINITION Sequence 4 from Patent WO9904266.
ACCESSION AX006172
VERSION AX006172.1 GI:9929052
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1

AUTHORS Smith, G.C. and Jackson, S.P.
TITLES Assays, therapeutic methods and means
JOURNAL Patent: WO 9904266-A 4 28-JAN-1999;
SMITH GRAEME CAMERON MURRAY (GB); CANCER RES CAMPAIGN TECH (GB)
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ORIGIN

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QY 1 CCCGAGAGCAGTCTGGC 18
DB 113 CCCGAGAGCAGTCTGGC 96

RESULT 25
LOCUS BD073938/c
DEFINITION Assay, remedy and remedy means.
ACCESSION BD073938
VERSION BD073938.1 GI:22619541
KEYWORDS JP 2001510684-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1303)
AUTHORS Lane, D.P., Jackson, S.P., Lakin, N.D. and Smith, G.C.M.
TITLES Assay, remedy and remedy means
JOURNAL Patent: JP 2001510684-A 2 07-AUG-2001;
KUDOS PHARMACEUTICALS LTD
OS Homo sapiens (human)
PN JP 2001510684-A/2
PD 07-AUG-2001
PF 16-JUL-1998 JP 2000503426
PR 16-JUL-1997 GB 9714971.0
PI DAVID PHILIP LANE, STEVEN PHILIP JACKSON, NICHOLAS DAVID LAKIN,
PI GRAHAM CAMERON MURRAY SMITH
PC C12N15/09, A61K38/00, A61P43/00, C07K14/82, C12N9/12, G01N33/15, PC
G01N33/50,
PC G01N33/56, C12N15/00, A61K37/02
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QY 1 CCCGAGAGCAGTCTGGC 18
DB 113 CCCGAGAGCAGTCTGGC 96

RESULT 26
LOCUS H00TP53B/c
DEFINITION Human p53 cellular tumor antigen mRNA, complete cds.
ACCESSION M14695
VERSION M14695.1 GI:333815
KEYWORDS antigen.

SOURCE	ORGANISM	Homosapiens (human)
REFERENCE	AUTHORS	Bukacynska, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. (bases 1 to 1303)
REFERENCE	AUTHORS	Harris, N., Brill, E., Shohat, O., Prokocimer, M., Wolf, D., Arari, N. and Rotter, V.
TITLE		Molecular basis for heterogeneity of the human p53 protein
JOURNAL		Mol. Cell. Biol. 6 (12), 4650-4656 (1986)
MEDLINE		87089826
PUBMED		3025664
COMMENT		Original source text: Human transformed cell line SV-80, cDNA to mRNA, clone p53-H-19.
FEATURES		Location/Qualifiers
source		1..1303
gene		/organism="Homo sapiens"
CDS		/mol_type="mRNA"
		/db_xref="taxon:9606"
		/map="17p13.1"
		1..1303
		/gene="TP53"
		122..1303
		/gene="TP53"
		/note="p53 antigen"
		/codon_start=1
		/protein_id="AAA61212.1"
		/db_xref="GI:339816"
		/db_xref="GBB:G000120-445"
		/translation="MEBPQSDPSVPEPLSGEPTSDMLKLLPENNVLSPLSPQAMDIDLMLSDPDLIEQWFTPEPDPGPDAPRMPRAAPVPAATPTPAAPAPASWPLSSVSQCTIYGSIGFRIGLHSGTAKSVCTISPLANKMFCQIAKTCFVQIMVDSITPPGIVRAMVAIKYSQNTAEVTRCRPHRSCSDSDGLAPQGLIVEGNLEVEYLDGRNFRHSVVVAPEPVSQDCTITHYNNCMNSCMGSMNRPLITITLEDSSGMLDGRNSEVAVCAACGRQRRTTEENLRKKGEPHEILPQSTKCALPNNSSPQPKKKPLDGEFTYQIGKGRREFEMFELNVALEIKDAQGKEPGGSRASHSLKSKKGQSTSRKTLMKTEGPDS"
ORIGIN		553 bp upstream of Pulli site; chromosome 17p13.
Query Match		100.0%; Score 18; DB 9; Length 1303;
Best Local Similarity		100.0%; Pred. No. 3.9e+02;
Matches 18; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
DB		113 CCGGGAAGGAGCTGGC 96
RESULT 27		1307 bp DNA linear PAT 07-OCT-1996
LOCUS		122242
122242/c		Sequence 12 from patent US 5527676.
DEFINITION		122242
ACCESSION		122242.1
VERSION		GI:1602596
KEYWORDS		Unknown.
SOURCE		Unclassified.
ORGANISM		1 (bases 1 to 1307)
REFERENCE		Vogelstein, B., Baker, S.J., Fearon, E.R. and Nigro, J.M.
AUTHORS		Detection of loss of the wild-type p53 gene and kites therefor
JOURNAL		Patent: US 5527676-A 12 18-JUN-1996;
FEATURES		Location/Qualifiers
source		1..1307
		/organism="unknown"
		/mol_type="unassigned DNA"
ORIGIN		100.0%; Score 18; DB 6; Length 1307;
Query Match		Best Local Similarity 100.0%; Pred. No. 3.8e+02;
Matches 18; Conservative		0; Mismatches 0; Indels 0; Gaps 0;
DB		1 CCGGGAAGGAGCTGGC 18

Db	117	CCCGAAGCGAGTCTGCG	100
RESULT 28			
HUMTP53a/c			
LOCUS		1307 bp	linear
DEFINITION		Human p53 cellular tumor antigen mRNA, complete cds.	PRI 14-JAN-1995
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
MEDLINE			
PUBMED			
COMMENT			
FEATURES			
source			
gene			
CDS			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
OR			
DB			
RESULT 29			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
Location/Qualifiers			

REFERENCE	Mammalia; Eutheria; Primates; Carnarhini; Homnidae; Homo.
AUTHORS	Thomann, H. U. and Fitzgerald, M. S.
TITLE	Rapid determination of gene structure using cDNA sequence
JOURNAL	Patent: WO 0153529-A 96 26-JUL-2001;
FEATURES	Genome Therapeutics Corporation (US)
source	Location/Qualifiers
	1. 1317
	/organism="Homo sapiens"
	/mol_type="unassigned DNA"
	/db_xref="taxon:9606"
ORIGIN	
Query Match	100.0%; Score 18; DB 6; Length 1317;
Best Local Similarity	100.0%; Pred. No. 3,8e+02;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CCCGGAAGGCACTTGGC 18
Db	127 CCCGGAAGGCACTTGGC 110
RESULT 39	
LOCUS	BD064183/c
DEFINITION	BD064183 1317 bp DNA linear PAT 27-AUG-2002
ACCESSION	Methods for targeting, enriching, detecting and/or isolating target
VERSION	BD064183
KEYWORDS	nucleic acid sequence using RecA-like recombinase.
SOURCE	BD064183.1 GI:22609786
ORGANISM	JP 2001506124-A/8.
	Conus quercinus
	Conus quercinus
	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
	Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
	Neogastropoda; Conoidea; Conidae; Conus.
REFERENCE	1 (bases 1 to 1317)
AUTHORS	Kigawa, K., Yamanaka, M., Kusumi, K., Mukai, E. and Obata, K.
TITLE	Methods for targeting, enriching, detecting and/or isolating target
JOURNAL	nucleic acid sequence using RecA-like recombinase
	Patent: JP 2001506124-A 8 15-MAY-2001;
DAIKIN INDUSTRIES LTD	
PN	JP 2001506124-A/8
PD	15-MAY-2001
PR	29-AUG-1997 JP 1996511481
PR	29-AUG-1996 JP 8/229061.26-DEC-1996 JP 8/347090 PI
KOUTI KITAWA, MIKAYO YAMANAKA, KAYO KUSUMI, ERI MUKAI, KAZUAKI PI	OBATA
PC	GI201/68
CC	Strandedness: Double;
CC	Topology: Linear;
FM	Key
FEATURES	Location/Qualifiers
source	1. 1317
	/organism="Conus quercinus"
	/mol_type="genomic DNA"
	/db_xref="taxon:101313"
ORIGIN	
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Best Local Similarity	100.0%; Pred. No. 3,8e+02;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CCCGGAAGGCACTTGGC 18
Db	127 CCCGGAAGGCACTTGGC 110
RESULT 40	
LOCUS	HSP53
DEFINITION	Human mRNA for p53 cellular tumor antigen.
ACCESSION	X02469 M60950
VERSION	X02469.1 GI:35209
	1317 bp mRNA linear PRI 12-SEP-1993

SOURCE	antigen; tumor antigen.
KEYWORDS	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1317) Zakut-Houri,R., Bienz-Tadnor,B., Givol,D. and Oren,M. Human p53 cellular tumor antigen: cDNA sequence and expression in COS cells
AUTHORS	EMBO J. 4 (5), 1251-1255 (1985)
TITLE	COS cells
JOURNAL	EMBO J. 4 (5), 1251-1255 (1985)
MEDLINE	85230577
PUBMED	4006916
COMMENT	Data kindly reviewed (19-FEB-1986) by D. Givol.
FEATURES	Location/Qualifiers
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	/mol_type="mRNA"
	/db_xref="taxon:9606"
	136..1317
	/note="unnamed protein product; p53 tumor antigen (aa 1-?)"
	/codon_start=1
	/protein_id="CAA26306.1"
	/db_xref="GI:35210"
	/db_xref="GOA:P04637"
	/db_xref="SWISS-PROT:P04637"
	/translation="MEEPQSDPSEPEPLLSQETFSDLMLKLPENNVLSPISQAMDLM LSPDIDQWTFEDGPDPEAPRMEPAAPVAPAAPATPAAPAPASPPSSVSQAK YQGSGPTFLHSCTASKVTCSFPAIKMKCOLAKTCPIOWIWDSPPGCTVRAM AIYKQSGMTBYVARCPHERCDSGLAPPOHLRVZGANRLVELIDRNTFRSVTV PYEPVGSDDCTTHIVYNCKNSCWGMGNRRPILITLEDSSGLIGRNSFEVCA CEPRARTBEENLNKKGEPHDELPGSTRAIPNNITSSPQPKKKPLDGVEFTLIQIRGA RERFMERLEINALELKDAQKGKEPSGRASHSHLKSXKQOSTSRHKLMFKTEGPDS D"
repeat_region	354..368
	/note="direct repeat 1"
repeat_region	384..398
	/note="direct repeat 1"
Query Match	100.0%; Score 18; DB 9; Length 1317;
Best Local Similarity	100.0%; Pred. No. 3.8e+02;
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy	1 CCCGAAAGCGCAGTGTGC 18
Db	127 CCCGAAAGCGCAGTGTGC 110
RESULT 41	
E13558/c	E13558
LOCUS	Mutated p53 gene. 1760 bp DNA linear PAT 27-APR-1998
DEFINITION	E13558
ACCESSION	E13558.1 GI:3252363
VERSION	JP 1997206070-A/1.
KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1760) Kawaguchi,R. and Hikichi,K. CELL-LINE ORIGINATED FROM HUMAN BONE MARROW CELLS Patent: JP 1997206070-A 1 12-AUG-1997;
REFERENCE	S R L:KK
AUTHORS	OS Homo sapiens (human)
TITLE	PN JP 1997206070-A/1
JOURNAL	PD 12-AUG-1997
	PF 31-JAN-1996 JP 1996037400
	PI KAWAGUCHI RYUJI,HIKICHI KAZUMASA
	PC C12N5/06,C07H21/04,C12N9/08//C12N15/09,C12Q1/68,(C12N5/06, PC C12R1/91);
	PC (C12N9/08,C12R1/91);

CC strandedness: Double;
CC topology: Linear;
FH Key Location/Qualifiers
FT
FT source 1..1760
FT /organism='Homo sapiens',
FT /cell_type='bone marrow-derived cell' FT
FT CDS 215..1396
FT /product='mutated p53',
FT mutation replace(957,'g')
FT mutation replace(1317,'a')
FT Location/Qualifiers
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Query Match 100.0%; Score 18; DB 6; Length 1760;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCGGAGGAGGAGTCTGGC 18
Db 206 CCGGAGGAGGAGTCTGGC 189

RESULT 42
E13737/c E13737 1760 bp DNA linear PAT 27-APR-1998
DEFINITION cDNA encoding human p53 protein which is as p53 cancer inhibitory gene product.
E13737
VERSION E13737.1 GI:3252505
KEYWORDS JP 1997229933-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1760)
Sugano, K. and Sacotte, K.
AUTANTIBODY DETECTING METHOD FOR P53 PROTEIN
Patent: JP 1997229933-A 1 05-SEP-1997;
SUGANO KOKICHI, NICHIREI CORP
OS Homo sapiens (human)
PN JP 1997229933-A/1
PD 05-SEP-1997
PF 27-FEB-1996 JP 1996124123
PI SUGANO KOKICHI, SAOTOME KEIICHI
PC G01N33/53, C07K14/47, C07K16/42, G01N33/564;
CC strandedness: Double;
CC topology: Linear;
CC hypothetical: No;
CC anti-sense: No;
FH Key Location/Qualifiers
FT source 1..1760
FT /organism='Homo sapiens',
FT /cell_line='WI-38VA13',
FT 5'UTR 1..214
FT CDS 215..1396
FT /product='human p53 protein which is as p53
FT cancer
FT inhibitory gene product',
FT 3'UTR 1397..1760.
FT Location/Qualifiers
1..1760
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/mol_type='genomic DNA'
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Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCGGAGGAGGAGTCTGGC 18
Db 206 CCGGAGGAGGAGTCTGGC 189

RESULT 43
BD084820/c BD084820 1760 bp DNA linear PAT 27-AUG-2002
LOCUS BD084820
DEFINITION Diagnosis method and reagents.
BD084820
ACCESSION BD084820.1 GI:22630430
VERSION JP 2001522241-A/13.
KEYWORDS JP 2001522241-A/13.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1760)
Leeuwen, F.W.V., Grosveld, F.G. and Burbach, V.P.H.
Diagnosis method and reagents
Patent: JP 2001522241-A 13 13-NOV-2001;
ROYAL NETHERLANDS ACADEMY OF ARTS AND SCIENCES, ERASMUS UNIVERSITY ROTTERDAM, UNIVERSITY OF UTRECHT
OS Homo sapiens (human)
PN JP 2001522241-A/13
PD 13-NOV-2001
PF 02-APR-1998 JP 1998542545
PR 10-APR-1997 US 60/043163
PI FREDERIK W VAN LEEUWEN, FRANKLIN G GROSVELD, JOHANNES PETER HENRI BURBACH
PC C12Q1/68, C07K14/47, C12N15/52, C12N9/00, C12N5/10, A61K38/43, PC A01K67/027,
PC A01K48/00//C07K16/18
CC Strandedness: Double;
CC topology: Linear;
CC p53 cellular tumor antigen gene; Genbank accession number CC K03199

FEATURES
source
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Location/Qualifiers
/organism='Homo sapiens'
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Query Match 100.0%; Score 18; DB 6; Length 1760;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCGGAGGAGGAGTCTGGC 18
Db 206 CCGGAGGAGGAGTCTGGC 189

RESULT 44
HUMPS3T/c HUMPS3T 1760 bp mRNA linear PRI 07-JAN-1995
LOCUS HUMPS3T
DEFINITION Human p53 cellular tumor antigen mRNA, complete cds.
HUMPS3T
ACCESSION K03199
VERSION K03199.1 GI:189478
KEYWORDS antigen; antigen p53.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1760)
Harlow, E.
Unpublished (1985)

REFERENCE		2 (bases 1 to 160)	
AUTHORS		Harrow E., Williamson N.M., Ralston R., Helfman D.M. and Adams T.B.	
TITLE		Molecular cloning and in vitro expression of a cDNA clone for human cellular tumor antigen p53	
JOURNAL		Mol. Cell. Biol. 5 (7), 1601-1610 (1985)	
MEDLINE		85267676	
PUBMED		3894933	
REFERENCE		3 (sites)	
AUTHORS		McBride O.W., Merry D. and Giyoil D.	
TITLE		The gene for human p53 cellular tumor antigen is located on chromosome 17 short arm (17p13)	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 83 (1), 130-134 (1986)	
MEDLINE		86094327	
PUBMED		3001719	
COMMENT		Original source text: Human vulva carcinoma (cell line A431), cDNA to mRNA, clone p4-2. [3] sites; chromosomal location. A draft entry and sequence for [2], [1] were kindly submitted via electronic mail by E.Harrow 17-OCT-1985. [1] reports that positions 1-79 may be a cloning artifact generated by ligating a second, unrelated cDNA to the 5' end of the p53 cDNA. Location/Qualifiers 1..1760 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /map="17p13.1" 1..1760 /gene="TP53" <1..>1760 /gene="TP53" /product="p53 mRNA" 215..1396 /gene="TP53" /note="p53 cellular tumor antigen" /codon_start=1 /protein_id="AA59989.1" /db_xref="GI:189479" /translation="MEPEQSDPSVEPPLSGETSPDLMKLLPENNYLSPLPSQADDMLMISPDIIEOMFTEDGDPDEAPMAPPAAPVAPAPAPAPAPASWPLSSVSQKTCYXGSYGFRLFGHSGLAKSVCTYSPLANNFCQLAKTCPVOLWDSTPPGTFRVLAAMAYKOSQMTEVRNCPHBERCDSGLAPPHOLLIVEGNLAEYLDRNFRRHSVVVPREPRFVSDCTTTHNYNMCKSSCMGSMNRPLITLTIEDSSGMLLRNSFEYHGKACCGGRRTTEENLRKGEPHEHLPGSITKALNNNTSSSPQEKSLDLGERIFTIQRKARRRFFEMRELNEALELKDAQAGKEPGGSRASHSLSKSGYSTSRKKLMFKETGGPPOS"	
ORIGIN	1 bp upstream of SalI site; Chromosome 17p13 [Unpublished (1985) C.		
Query Match	100.0%; Score 18; DB 9; Length 1760;		
Best Local Similarity	100.0%; Pred. No. 3.5e+02;		
Matches	18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
CY	1 CCCGAAGGCAGCTGGC 18 		
Ddb	206 CCCGAAGGCAGCTGGC 189		
RESULT 45			
LOCUS	AF192534/c	2355 bp DNA linear SYN 19-APR-20000	
DEFINITION	Expression vector Ad5CMV-p53 tumor suppressor protein p53 (p53)		
ACCESSION	AF192534	expression cassette, complete sequence.	
VERSION	AF192534.1	GI:7595311	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

TITLE

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

FEATURES
source

gene
CDS

ORIGIN

Query Match Best Local Similarity Matches Oy Db

RESULT_46 LOCUS DEFINITION ACCESSION VERSION KEYWORDS ORGANISM SOURCE REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE

liposome-mediated transfection and PCR analysis
Biotechniques 15 (5), 868-872 (1993)
94092464
8267983
2 (bases 1 to 2355)
Zhang,W.W., Fang,X., Mazur,W., French,B.A., Georges,R.N. and Roth,J.A.
High-efficiency gene transfer and high-level expression of wild-type p53 in human lung cancer cells mediated by recombinant adenovirus
Cancer Gene Ther. 1 (1), 5-13 (1994)
95346687
7621238
3 (bases 1 to 2355)
Huet,T., Wilson,D.R., Zhang,W.W. and Roth,J.A.
Direct Submission
Submitted (06-OCT-1999) Oncology, Rhone-Poulenc Rorer Gencell, 38235 Bay Center Place, Hayward, CA 94545, USA
Location/Qualifiers
1..2355
/organism="Expression vector Ad5CMV-p53"
/mol_type="Genomic DNA"
/db_xref="taxon:120786"
/note="p53 expression cassette of RPR/INGN 201 recombinant adenovirus vector. Artificial sequence; contains CMV promoter and the SV40 polyadenylation signal"
921..2102
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/product="tumor suppressor protein p53"
/protein_id="AA64408.1"
/db_xref="GI:7595312"
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100.0%; Score 18; DB 12; Length 2355;
100.0%; Pred. No. 3.3e+02;
18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCCGAAGCGACTGTGC 18
|||||
|||
912 CCCGAAGCGACTGTGCC 895

AB082923 2451 bp mRNA linear PRI 01-APR-2003
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Homo sapiens (human)

AB082923 2451 bp mRNA linear PRI 01-APR-2003
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

AB082923.1 GI:23491728

1
Aama,K., Shichio,S., Maeda,Y., Nakasaur,T., Nonaka,Y., Fujii,T.,
Koike,K. and Itoh,K.
Mutated p53 gene encodes a nonmutated epitope recognized by HLA-B*4601-restricted and tumor cell-reactive CTLs at tumor site
Cancer Res. 63 (4), 854-858 (2003)
22479085
12591737
2 (bases 1 to 2451)

MEDLINE	93303270
PUBMED	8316528
REFERENCE	2 (bases 1 to 3423)
AUTHORS	Anderson,C.W. and Allalunis-Turner,M.J.
TITLE	Human T53 from the malignant glioma-derived cell lines M059J and M059K has a cancer-associated mutation in exon 8
JOURNAL	Radiat. Res. 154 (4), 473-476 (2000)
MEDLINE	20476181
PUBMED	11023613
REFERENCE	3 (bases 1 to 3423)
AUTHORS	Anderson,C.W., Kieleczawa,J. and Allalunis-Turner,M.J.
TITLE	Direct Submission
JOURNAL	Submitted (16-MAR-1999) Biology, Brookhaven National Laboratory, 500 Bell Avenue, Upton, NY 11973-5000, USA
FEATURES	Location/Qualifiers
source	1..3423

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CM nucleic - nucleic search, using sw model

Run on: March 2, 2004, 03:28:11 / Search time 269 Seconds
(without alignments)
241.392 Million cell updates/sec

Title: US-09-848-868-35

Perfect score: 18 cccggaagcagctctgac 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 2353733 seqs, 1803733377 residues

Total number of hits satisfying chosen parameters: 4707466

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database:

Published Applications NA:*

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- 2: /cgm2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgm2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgm2_6/prodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgm2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgm2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgm2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*
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- 11: /cgm2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
- 12: /cgm2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgm2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 14: /cgm2_6/prodata/2/pubpna/US10_PUBCOMB.seq:*
- 15: /cgm2_6/prodata/2/pubpna/US10C_PUBCOMB.seq:*
- 16: /cgm2_6/prodata/2/pubpna/US10C_NEW_PUB.seq:*
- 17: /cgm2_6/prodata/2/pubpna/US60_NEW_PUB.seq:*
- 18: /cgm2_6/prodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	10	US-09-848-868-35
2	18	100.0	35	10	US-09-848-868-36
3	18	100.0	133	9	US-09-776-695-42
4	18	100.0	1303	15	US-10-397-635-6
5	18	100.0	1307	9	US-09-732-384-6
6	18	100.0	1317	10	US-09-829-922-1
7	18	100.0	1317	14	US-10-160-290-1
8	18	100.0	1760	10	US-09-849-602-9
9	18	100.0	1760	15	US-10-191-121-4
10	18	100.0	2209	15	US-10-062-674-2065
11	18	100.0	2521	15	US-10-429-802-25
12	18	100.0	2521	15	US-10-430-503-16
13	18	100.0	2625	12	US-10-391-068-1
14	18	100.0	2629	14	US-10-077-176-58
15	18	100.0	2629	14	US-10-077-176-59
71	15.4	85.6	1290	12	US-10-284-124A-0053
72	15.4	85.6	1491	10	US-09-925-301-138
73	15.4	85.6	1717	10	US-09-960-706-953
74	15.4	85.6	1717	10	US-09-873-319-623
75	15.4	85.6	1717	14	US-10-171-311-118
76	15.4	85.6	1717	14	US-10-301-822-108
77	15.4	85.6	1772	14	US-10-210-101-68
78	15.4	85.6	1804	14	US-10-175-152-137
79	15.4	85.6	1804	15	US-10-159-566-255
80	15.4	85.6	1826	14	US-10-106-698-318
81	15.4	85.6	1889	12	US-10-102-412-13157
82	15.4	85.6	2875	14	US-10-101-510-354
83	15.4	85.6	2876	15	US-10-062-674-1963
84	15	83.3	215	9	US-09-994-093B-3015
85	15	83.3	3112	12	US-10-425-114-22028
86	15	83.3	1691139	14	US-10-067-514-1
87	15	83.3	1591139	15	US-10-419-723-1
88	14.8	82.2	108	14	US-10-123-807-21
71	15.4	85.6	1290	12	Sequence 2083, App
72	15.4	85.6	1491	10	Sequence 138, App
73	15.4	85.6	1717	10	Sequence 953, App
74	15.4	85.6	1717	10	Sequence 621, App
75	15.4	85.6	1717	14	Sequence 118, App
76	15.4	85.6	1717	14	Sequence 108, App
77	15.4	85.6	1772	14	Sequence 68, App
78	15.4	85.6	1804	14	Sequence 177, App
79	15.4	85.6	1804	15	Sequence 326, App
80	15.4	85.6	1826	14	Sequence 375, App
81	15.4	85.6	1889	12	Sequence 35157, A
82	15.4	85.6	2875	14	Sequence 364, App
83	15.4	85.6	2876	15	Sequence 1663, App
84	15	83.3	215	9	Sequence 3015, Ap
85	15	83.3	3112	12	Sequence 22028, A
86	15	83.3	1691139	14	Sequence 1, Appli
87	15	83.3	1591139	15	Sequence 1, Appli
88	14.8	82.2	108	14	Sequence 59, Appl
89	14.8	82.2	108	14	Sequence 21, Appl

89 14.8 82.2 563 15 US-10-027-632-84156 Sequence 84156, A
90 14.8 82.2 617 15 US-10-027-632-261398 Sequence 261398,
91 14.8 82.2 617 15 US-10-027-632-261399 Sequence 261399,
92 14.8 82.2 727 15 US-10-027-632-261400 Sequence 261400,
93 14.8 82.2 727 15 US-10-027-632-50560 Sequence 50560, A
94 14.8 82.2 730 15 US-10-027-632-13823 Sequence 13823, A
95 14.8 82.2 820 15 US-10-027-632-168125 Sequence 168125,
96 14.8 82.2 820 15 US-10-027-632-168126 Sequence 168126,
97 14.8 82.2 820 15 US-10-027-632-168127 Sequence 168127,
98 14.8 82.2 820 15 US-10-027-632-168128 Sequence 168128,
99 14.8 82.2 823 15 US-10-027-632-128849 Sequence 128849,
100 14.8 82.2 838 15 US-10-027-632-172737 Sequence 172737,

ALIGNMENTS

RESULT 1
US-09-848-868-35
Sequence 35, Application US/09848868
Publication No. US2003016588A1
GENERAL INFORMATION:
APPLICANT: Iversen, Patrick L.
TITLE OF INVENTION: Splice-Region Antisense Composition and
FILE REFERENCE: 0450-0037.30
CURRENT APPLICATION NUMBER: US/09/848, 868
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/202,376
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense
US-09-848-868-35

Query Match 100.0%; Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTGTGGC 18
DB 1 CCGGAGGCGAGTGTGGC 18

RESULT 2
US-09-848-868-36
Sequence 36, Application US/09848868
Publication No. US2003016588A1
GENERAL INFORMATION:
APPLICANT: Iversen, Patrick L.
TITLE OF INVENTION: Splice-Region Antisense Composition and
FILE REFERENCE: 0450-0037.30
CURRENT APPLICATION NUMBER: US/09/848, 868
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/202,376
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense
US-09-848-868-36

Query Match 100.0%; Score 18; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTGTGGC 18
DB 17 CCGGAGGCGAGTGTGGC 34

RESULT 3
US-09-776-695-22/c
Sequence 22, Application US/09776695
Patent No. US20020068283A1
GENERAL INFORMATION:
APPLICANT: Boeke, Jef
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING P53
MUTATIONS WHICH SUPPRESS P53 CANCER MUTA- TIONS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Wilcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/776, 695
FILING DATE: 26-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795, 006
FILING DATE: 2001-03-28
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.03170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-776-695-22

Query Match 100.0%; Score 18; DB 9; Length 133;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTGTGGC 18
DB 35 CCGGAGGCGAGTGTGGC 18

RESULT 4
US-10-397-635-6/c
Sequence 6, Application US/10397635
Publication No. US2004000604A1
GENERAL INFORMATION:
APPLICANT: ZHANG, XIAOLIU
TITLE OF INVENTION: POTENT ONCOLYTIC HERPES SIMPLEX VIRUS FOR CANCER

```

PRIORITY FILING DATE: 1995-02-16
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1317
TYPE: DNA
ORGANISM: Homo sapiens
US-09-829-922-1

Query Match          100.0%; Score 18; DB 10; Length 1317;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 18; Conservative 0; Indels 0; Gaps 0

      1  CCCGGAGGCGAGCTGGC 18
      |||
Db      127  CCCGGAGGCGAGCTGGC 110

RESULT 7
US-10-160-290-1/c
Sequence 1, Application US/10160290
Publication No. US20030124557A1
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos
Hartwig, Wolfgang
TITLE OF INVENTION: Peptides and Peptidomimetics with
Structural Similarity to Human p53 That Activate
p53
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/160,290
FILING DATE: 04-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/685,027
FILING DATE: 10-Oct-2000
APPLICATION NUMBER: 08/392,542
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 0486,48439
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-160-290-1

Query Match          100.0%; Score 18; DB 14; Length 1317;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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QY 1 CCCGAGAGCAGCTGTGGC 18
|||
Db 127 CCCGAGAGCAGCTGTGGC 110

RESULT 8
US-09-849-602-9/c
; Sequence 9, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: L0461/7105 (JMV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-849-602-9

Query Match 100.0%; Score 18; DB 10; Length 1760;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTGTGGC 18
|||
Db 206 CCCGAGAGCAGCTGTGGC 189

RESULT 9
US-10-191-121-4/c
; Sequence 4, Application US/10191121
; Publication No. US20040005574A1
; GENERAL INFORMATION:
; APPLICANT: Guarente, Leonard
; APPLICANT: Vaziri, Homayoun
; APPLICANT: Imai, Shin-Ichiro
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: Sir2 and p53 Deacetylation
; FILE REFERENCE: 13407-015002
; CURRENT APPLICATION NUMBER: US/10/191,121
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: US 60/303,456
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: US 10/NNN,NNN
; PRIOR FILING DATE: 2002-07-05
; PRIOR APPLICATION NUMBER: US 60/303,370
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-191-121-4

Query Match 100.0%; Score 18; DB 15; Length 1760;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTGTGGC 18
|||
Db 206 CCCGAGAGCAGCTGTGGC 189

RESULT 10

US-10-062-674-2065/c
; Sequence 2065, Application US/10062674
; Publication No. US20040005559A1
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.; Kaser, Matthew R.
; TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
; FILE REFERENCE: PA-0026-1 CIP
; CURRENT APPLICATION NUMBER: US/10/062,674
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: US 09/625,102
; PRIOR FILING DATE: 2000-07-24
; NUMBER OF SEQ ID NOS: 2217
; SOFTWARE: PERL Program
; SEQ ID NO 2065
; LENGTH: 2209
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040005559A1 430224.2
US-10-062-674-2065

Query Match 100.0%; Score 18; DB 15; Length 2209;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTGTGGC 18
|||
Db 170 CCCGAGAGCAGCTGTGGC 153

RESULT 11
US-10-429-802-25/c
; Sequence 25, Application US/10429802
; Publication No. US20030228285A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: WONG, KA YIN
; APPLICANT: ZOU, YIYU
; TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
; FILE REFERENCE: UTSQ:752US
; CURRENT APPLICATION NUMBER: US/10/429,802
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/377,672
; PRIOR FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 2521
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-429-802-25

Query Match 100.0%; Score 18; DB 15; Length 2521;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTGTGGC 18
|||
Db 127 CCCGAGAGCAGCTGTGGC 110

RESULT 12
US-10-430-503-16/c
; Sequence 16, Application US/10430503
; Publication No. US20040005684A1
; GENERAL INFORMATION:
; APPLICANT: HUNG, MIEN-CHIE
; APPLICANT: LAN, KENG-LI
; APPLICANT: OU-YANG, FU
; APPLICANT: LIU, JAW-CHING
; APPLICANT: LAN, KENG-CHIN
; TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC

```
/ TITLE OF INVENTION: REAGENTS
/ FILE REFERENCE: UTSC:797US
/ CURRENT APPLICATION NUMBER: US/10/430,503
/ CURRENT FILING DATE: 2003-05-06
/ PRIORITY APPLICATION NUMBER: 60/383,063
/ PRIORITY FILING DATE: 2002-05-06
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 2521
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-430-503-16

Query Match      100.0%; Score 18; DB 15; Length 2521;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGCTGGC 18
Db 127 CCGGAGGCGAGCTGGC 110

RESULT 13
US-10-391-068-1/c
/ Sequence 1, Application US/10391068
/ Publication No. US20040028654A1
/ GENERAL INFORMATION:
/ APPLICANT: JI, LIN
/ APPLICANT: ROTH, JACK
/ TITLE OF INVENTION: PROTAMINE-ADENOVIIRAL VECTOR COMPLEXES
/ TITLE OF INVENTION: AND METHODS OF USE
/ FILE REFERENCE: INRP:097US
/ CURRENT APPLICATION NUMBER: US/10/391,068
/ CURRENT FILING DATE: 2003-03-24
/ PRIORITY APPLICATION NUMBER: 60/366,846
/ PRIORITY FILING DATE: 2002-03-22
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 2625
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATUERS:
/ NAME/KEY: CDS
/ LOCATION: (252) ..(1433)
US-10-391-068-1

Query Match      100.0%; Score 18; DB 12; Length 2625;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGCTGGC 18
Db 243 CCGGAGGCGAGCTGGC 226

RESULT 14
US-10-077-176-58/c
/ Sequence 59, Application US/10077176
/ Publication No. US20030175862A1
/ GENERAL INFORMATION:
/ APPLICANT: Brachmann, Rainer
/ TITLE OF INVENTION: ENGINEERED OPEN READING FRAME FOR P53
/ FILE REFERENCE: 004255.00008
/ CURRENT APPLICATION NUMBER: US/10/077,176
/ CURRENT FILING DATE: 2002-02-19
/ NUMBER OF SEQ ID NOS: 71
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 58
/ LENGTH: 2629
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/
```

```
US-10-077-176-58

Query Match      100.0%; Score 18; DB 14; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGCTGGC 18
Db 243 CCGGAGGCGAGCTGGC 226

RESULT 15
US-10-077-176-59/c
/ Sequence 59, Application US/10077176
/ Publication No. US20030175862A1
/ GENERAL INFORMATION:
/ APPLICANT: Brachmann, Rainer
/ TITLE OF INVENTION: ENGINEERED OPEN READING FRAME FOR P53
/ FILE REFERENCE: 004255.00008
/ CURRENT APPLICATION NUMBER: US/10/077,176
/ CURRENT FILING DATE: 2002-02-19
/ NUMBER OF SEQ ID NOS: 71
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 59
/ LENGTH: 2629
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-077-176-59

Query Match      100.0%; Score 18; DB 14; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGCTGGC 18
Db 243 CCGGAGGCGAGCTGGC 226

RESULT 16
US-10-077-176-60/c
/ Sequence 60, Application US/10077176
/ Publication No. US20030175862A1
/ GENERAL INFORMATION:
/ APPLICANT: Brachmann, Rainer
/ TITLE OF INVENTION: ENGINEERED OPEN READING FRAME FOR P53
/ FILE REFERENCE: 004255.00008
/ CURRENT APPLICATION NUMBER: US/10/077,176
/ CURRENT FILING DATE: 2002-02-19
/ NUMBER OF SEQ ID NOS: 71
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 60
/ LENGTH: 2629
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-077-176-60

Query Match      100.0%; Score 18; DB 14; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGCTGGC 18
Db 243 CCGGAGGCGAGCTGGC 226

RESULT 17
US-10-077-176-61/c
/ Sequence 61, Application US/10077176
/ Publication No. US20030175862A1
/ GENERAL INFORMATION:
/ APPLICANT: Brachmann, Rainer
/ TITLE OF INVENTION: ENGINEERED OPEN READING FRAME FOR P53
/ FILE REFERENCE: 004255.00008
/
```

;; CURRENT APPLICATION NUMBER: US/10/077,176
;; CURRENT FILING DATE: 2002-02-19
;; NUMBER OF SEQ ID NOS: 71
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 61
;; LENGTH: 2629
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-077-176-61

Query Match 100.0%; Score 18; DB 14; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 243 CCGGAGGCGAGTCTGGC 226

RESULT 18
US-10-439-388-16/c
;; Sequence 16, Application US/10439388
;; Publication No. US20030228617A1
;; GENERAL INFORMATION:
;; APPLICANT: Aune, Thomas M
;; APPLICANT: Olsen, Nancy J
;; TITLE OF INVENTION: Method for Predicting Autoimmune Disease
;; FILE REFERENCE: 1242/58
;; CURRENT APPLICATION NUMBER: US/10/439,388
;; CURRENT FILING DATE: 2003-05-16
;; PRIOR APPLICATION NUMBER: US 60/381,055
;; PRIOR FILING DATE: 2002-05-16
;; NUMBER OF SEQ ID NOS: 70
;; SOFTWARE: PatentIn version 3.2
;; SEQ ID NO 16
;; LENGTH: 2629
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-439-388-16

Query Match 100.0%; Score 18; DB 15; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 243 CCGGAGGCGAGTCTGGC 226

RESULT 19
US-10-165-216-3/c
;; Sequence 3, Application US/10165216
;; Publication No. US20030228675A1
;; GENERAL INFORMATION:
;; APPLICANT: O'Brien, Diane M.
;; APPLICANT: Abraham, Robert T.
;; TITLE OF INVENTION: ATM Related Kinase ATRX, Nucleic Acids
;; FILE REFERENCE: P-LJ 5222
;; CURRENT APPLICATION NUMBER: US/10/165,216
;; CURRENT FILING DATE: 2002-06-06
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 2629
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (252)...(1433)
US-10-165-216-3

Query Match 100.0%; Score 18; DB 15; Length 2629;

Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 243 CCGGAGGCGAGTCTGGC 226

RESULT 20
US-10-159-563-188/c
;; Sequence 188, Application US/10159563
;; Publication No. US20040009154A1
;; GENERAL INFORMATION:
;; APPLICANT: Khan, Javed
;; APPLICANT: Ringner, Markus
;; APPLICANT: Peterson, Carsten
;; APPLICANT: Meltzer, Paul
;; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
;; TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
;; FILE REFERENCE: 11613.56US11
;; CURRENT APPLICATION NUMBER: US/10/159,563
;; CURRENT FILING DATE: 2002-12-09
;; PRIOR APPLICATION NUMBER: US 10/133,937
;; PRIOR FILING DATE: 2002-04-25
;; NUMBER OF SEQ ID NOS: 444
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 188
;; LENGTH: 2629
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-10-159-563-188

Query Match 100.0%; Score 18; DB 15; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 243 CCGGAGGCGAGTCTGGC 226

RESULT 21
US-09-918-995-36880/c
;; Sequence 36880, Application US/09918995
;; Publication No. US20030073623A1
;; GENERAL INFORMATION:
;; APPLICANT: Hyseq, Inc.
;; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
;; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
;; FILE REFERENCE: 20411-756
;; CURRENT APPLICATION NUMBER: US/09/918,995
;; CURRENT FILING DATE: 2001-07-30
;; PRIOR APPLICATION NUMBER: US/09/235,076
;; PRIOR FILING DATE: 1999-01-20
;; NUMBER OF SEQ ID NOS: 38054
;; SOFTWARE: FASTSEQ for Windows Version 3.0
;; SEQ ID NO 36880
;; LENGTH: 436
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-918-995-36880

Query Match 91.1%; Score 16.4; DB 10; Length 436;
Best Local Similarity 94.4%; Pred. No. 35;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 90 CCGGAGGCGAGTCTGGC 73

RESULT 22
US-10-066-543-113/c

```
/ Sequence 113, Application US/10066543
/ Publication No. US20030087818A1
/ GENERAL INFORMATION:
/ APPLICANT: Jiang, Yudiu
/ APPLICANT: Pyle, Ruth A.
/ APPLICANT: Xu, Jianshun
/ APPLICANT: Inditias, Carol Yoseph
/ APPLICANT: Lodes, Michael J.
/ APPLICANT: Secrist, Heather
/ APPLICANT: Carter, Darick
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Smith, Carole L.
/ APPLICANT: Durham, Margerita
/ APPLICANT: Stolk, John A.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
/ FILE REFERENCE: 210121.563
/ CURRENT APPLICATION NUMBER: US/10/066,543
/ CURRENT FILING DATE: 2002-01-31
/ NUMBER OF SEQ ID NOS: 3417
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 113
/ LENGTH: 905
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc.feature
/ LOCATION: 13, 45, 386, 545, 580, 582, 584, 590, 591, 603, 606, 609,
/ LOCATION: 610, 616, 621, 623, 624, 625, 629, 630, 646, 652, 670, 672,
/ LOCATION: 674, 676, 688, 700, 709, 710, 744, 753, 756, 758, 759, 763,
/ LOCATION: 786, 796, 823, 851, 876, 885
/ OTHER INFORMATION: n = A,T,C or G
US-10-066-543-113

Query Match          91.1%; Score 16.4; DB 14; Length 905;
Best Local Similarity 94.4%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGAGGCGAGTCTGGC 18
DB 516 CCCGAGGCGAGTCTGGC 499

RESULT 23
US-09-764-847-1845/C
/ Sequence 1845, Application US/09764847
/ Patent No. US20020132767A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PC009
/ CURRENT APPLICATION NUMBER: US/09/764,847
/ CURRENT FILING DATE: 2001-01-17
/ Prior application data removed - consult PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 2003
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1845
/ LENGTH: 942
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-764-847-1845

Query Match          91.1%; Score 16.4; DB 9; Length 942;
Best Local Similarity 94.4%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGAGGCGAGTCTGGC 18
DB 58 CCCGAGGCGAGTCTGTC 41
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RESULT 24
US-09-764-847-1846/C

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/ Sequence 1846, Application US/09764847
/ Patent No. US20020132767A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PC009
/ CURRENT APPLICATION NUMBER: US/09/764,847
/ CURRENT FILING DATE: 2001-01-17
/ Prior application data removed - consult PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 2003
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1846
/ LENGTH: 942
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-764-847-1846

Query Match          91.1%; Score 16.4; DB 9; Length 942;
Best Local Similarity 94.4%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGAGGCGAGTCTGGC 18
DB 58 CCCGAGGCGAGTCTGTC 41

RESULT 25
US-10-092-154-1845/C
/ Sequence 1845, Application US/10092154
/ Publication No. US20030054375A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PC009C1
/ CURRENT APPLICATION NUMBER: US/10/092,154
/ CURRENT FILING DATE: 2002-03-07
/ NUMBER OF SEQ ID NOS: 2003
/ Prior application removed - See File Wrapper or Palm
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1845
/ LENGTH: 942
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-092-154-1845

Query Match          91.1%; Score 16.4; DB 14; Length 942;
Best Local Similarity 94.4%; Pred. No. 50;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGAGGCGAGTCTGGC 18
DB 58 CCCGAGGCGAGTCTGTC 41

Search completed: March 2, 2004, 04:51:58
Job time : 273 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 1, 2004, 21:35:15 ; Search time 48 Seconds
(without alignments)

208.107 Million cell updates/sec

Title: US-09-848-868-35

Perfect score: 18

Sequence: 1 cccgaagcagctcggc 18

Scoring table: IDENTITY NUC

Gapop 10-0, Gapex 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents NA:*

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2: /cgn2_6/ptodata/2/ina/5B COMB.seg:*

3: /cgn2_6/ptodata/2/ina/6A COMB.seg:*

4: /cgn2_6/ptodata/2/ina/6B COMB.seg:*

5: /cgn2_6/ptodata/2/ina/PCrUS COMB.seg:*

6: /cgn2_6/ptodata/2/ina/backfile1.seg:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	102	1	US-08-047-041A-15
2	18	100.0	133	1	US-08-047-041A-2
3	18	100.0	133	2	US-08-795-006A-22
4	18	100.0	133	3	US-09-184-073-22
5	18	100.0	800	1	US-08-472-239-1
6	18	100.0	1070	3	US-09-414-436-4
7	18	100.0	1303	1	US-08-047-041A-13
8	18	100.0	1307	1	US-08-047-041A-12
9	18	100.0	1317	1	US-07-912-011-1
10	18	100.0	1317	1	US-08-347-792-1
11	18	100.0	1317	1	US-08-431-357-1
12	18	100.0	1317	2	US-08-697-221-1
13	18	100.0	1317	3	US-08-392-542-1
14	18	100.0	1317	3	US-08-884-327-1
15	18	100.0	1317	4	US-08-147-751-8
16	18	100.0	1317	4	US-09-305-914-1
17	18	100.0	1317	4	US-09-685-927-1
18	18	100.0	1317	5	PCT-US95-15353-1
19	15.4	85.6	184	4	US-09-404-879A-332
20	15.4	85.6	447	4	US-09-702-705-1634
21	15.4	85.6	447	4	US-09-736-057-1634
22	15.4	85.6	447	4	US-08-614-124B-1634
23	15.4	85.6	447	4	US-09-671-325-1634
24	15.4	85.6	633	3	US-09-385-982-206
25	15.4	85.6	647	4	US-09-222-575-81
26	15.4	85.6	647	4	US-09-389-681-81
27	15.4	85.6	647	4	US-09-620-405B-81

28	15.4	85.6	647	4	US-09-339-338-81	Sequence 81, Appl
29	15.4	85.6	647	4	US-09-433-826B-81	Sequence 81, Appl
30	15.4	85.6	647	4	US-09-604-287A-81	Sequence 81, Appl
31	15.4	85.6	647	4	US-09-285-480-81	Sequence 81, Appl
32	15.4	85.6	647	4	US-09-834-758-81	Sequence 81, Appl
33	15.4	85.6	25	1	US-08-447-179-7	Sequence 7, Appl
34	14.8	82.2	108	4	US-09-445-247-21	Sequence 21, Appl
35	14.8	82.2	1757	5	US-08-094-071-1	Sequence 1, Appl
36	14.8	82.2	1757	5	PCT-US92-00878-1	Sequence 1, Appl
37	14.8	82.2	8078	3	US-08-870-126-12	Sequence 12, Appl
38	14.8	82.2	8078	4	US-09-445-247-12	Sequence 12, Appl
39	14.8	82.2	14985	1	US-08-652-972A-6	Sequence 6, Appl
40	14.8	82.2	14985	5	PCT-US96-06231A-6	Sequence 6, Appl
41	14.8	82.2	4403765	3	US-09-103-840A-2	Sequence 2, Appl
42	14.8	82.2	4411529	4	US-09-103-840A-1	Sequence 1, Appl
43	14.4	80.0	252	3	US-09-621-976-11048	Sequence 11048, A
44	14.4	80.0	360	1	US-08-256-077-3	Sequence 3, Appl
45	14.4	80.0	360	1	US-08-466-127-1	Sequence 1, Appl
46	14.4	80.0	982	1	US-08-256-077-1	Sequence 1, Appl
47	14.4	80.0	982	1	US-08-466-127-1	Sequence 1, Appl
48	14.4	80.0	8137	1	US-09-566-921-7	Sequence 1, Appl
49	13.8	76.7	157	3	US-08-721-986-1	Sequence 1, Appl
50	13.8	76.7	157	3	US-08-225-487A-1	Sequence 28, Appl
51	13.8	76.7	212	1	US-08-435-684A-28	Sequence 28, Appl
52	13.8	76.7	212	1	US-08-934-877A-28	Sequence 28, Appl
53	13.8	76.7	212	3	US-08-871-678C-28	Sequence 28, Appl
54	13.8	76.7	237	4	US-09-552-931A-10772	Sequence 35, Appl
55	13.8	76.7	371	4	US-08-585-593A-35	Sequence 35, Appl
56	13.8	76.7	441	4	US-08-914-375C-53	Sequence 53, Appl
57	13.8	76.7	579	4	US-09-404-879A-188	Sequence 188, Appl
58	13.8	76.7	579	4	US-09-338-933-188	Sequence 188, Appl
59	13.8	76.7	579	4	US-09-215-681-188	Sequence 188, Appl
60	13.8	76.7	579	4	US-09-216-003A-188	Sequence 188, Appl
61	13.8	76.7	584	4	US-09-404-879A-187	Sequence 187, Appl
62	13.8	76.7	584	4	US-09-338-933-187	Sequence 187, Appl
63	13.8	76.7	584	4	US-09-215-681-187	Sequence 187, Appl
64	13.8	76.7	584	4	US-09-216-003A-187	Sequence 187, Appl
65	13.8	76.7	627	1	US-09-489-039A-2235	Sequence 2235, Ap
66	13.8	76.7	630	1	US-08-527-227A-5	Sequence 5, Appl
67	13.8	76.7	635	4	US-09-643-597-208	Sequence 208, Appl
68	13.8	76.7	635	4	US-09-480-884A-208	Sequence 208, Appl
69	13.8	76.7	655	4	US-09-542-615A-208	Sequence 208, Appl
70	13.8	76.7	655	4	US-09-606-421B-208	Sequence 208, Appl
71	13.8	76.7	690	4	US-09-328-352-3319	Sequence 3319, Ap
72	13.8	76.7	732	4	US-09-886-319A-81	Sequence 54, Appl
73	13.8	76.7	771	4	US-09-328-352-3448	Sequence 3448, Ap
74	13.8	76.7	834	1	US-08-166-195A-1	Sequence 1, Appl
75	13.8	76.7	834	1	US-08-436-775-1	Sequence 1, Appl
76	13.8	76.7	854	1	US-08-436-883B-1	Sequence 1, Appl
77	13.8	76.7	855	4	US-09-252-991A-10688	Sequence 10688, A
78	13.8	76.7	855	4	US-09-894-844-46	Sequence 46, Appl
79	13.8	76.7	987	4	US-09-252-991A-15247	Sequence 15247, A
80	13.8	76.7	993	4	US-09-833-381-895	Sequence 895, Appl
81	13.8	76.7	1001	4	US-09-671-311-230	Sequence 230, Appl
82	13.8	76.7	1001	4	US-09-671-311-231	Sequence 231, Appl
83	13.8	76.7	1032	4	US-09-016-433-1338	Sequence 1338, Ap
84	13.8	76.7	1116	4	US-09-252-991A-15444	Sequence 15444, A
85	13.8	76.7	1290	4	US-09-107-532A-3539	Sequence 3539, Ap
86	13.8	76.7	1344	4	US-09-252-991A-15551	Sequence 15551, A
87	13.8	76.7	1355	4	US-09-489-038A-439	Sequence 439, Appl
88	13.8	76.7	1355	4	US-09-252-991A-11115	Sequence 11115, A
89	13.8	76.7	1403	2	US-08-202-044-1	Sequence 1, Appl
90	13.8	76.7	1403	3	US-08-751-344B-1	Sequence 1, Appl
91	13.8	76.7	1403	4	US-09-920-868A-1	Sequence 1, Appl
92	13.8	76.7	1403	3	US-09-255-366-1	Sequence 1, Appl
93	13.8	76.7	1413	4	US-09-252-991A-11233	Sequence 11233, A
94	13.8	76.7	1446	4	US-09-252-991A-10948	Sequence 10948, A
95	13.8	76.7	1474	1	US-08-466-980-1	Sequence 1, Appl
96	13.8	76.7	1474	2	US-09-033-303-1	Sequence 1, Appl
97	13.8	76.7	1474	2	US-09-339-115-1	Sequence 1, Appl
98	13.8	76.7	1474	5	PCT-US95-07093-1	Sequence 1, Appl
99	13.8	76.7	1633	4	US-09-061-154-1	Sequence 1, Appl
100	13.8	76.7	1633	4	US-09-061-154-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-047-041A-15/c
Sequence 15, Application US/08047041A
Patent No. 5527676
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detection of loss of the wild-type p53
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,041A
FILING DATE: 22-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446,584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107,42917
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: exon 2
PUBLICATION INFORMATION:
AUTHORS: Lamb,
JOURNAL: Mol. Cell. Biol.
VOLUME: 6
ISSUE: 5
PAGES: 1379-1385
DATE: 1986
US-08-047-041A-15

Query Match 100.0%; Score 18; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 3.8;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCGGAGGAGCTCTG3C 18
Db 20 CCGGAGGAGCTCTG3C 3

RESULT 2
US-08-047-041A-2/c
Sequence 2, Application US/08047041A
Patent No. 5527676
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detection of loss of the wild-type p53
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,041A
FILING DATE: 22-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446,584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107,42917
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: exon 2
PUBLICATION INFORMATION:
AUTHORS: Buchman, V. L.
TITLE: A variation in the structure of the
TITLE: protein-coding region of the human p53 gene
JOURNAL: Gene
VOLUME: 70
PAGES: 245-252
DATE: 1988
US-08-047-041A-2

Query Match 100.0%; Score 18; DB 1; Length 133;

Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGAGCTGTGGC 18
DB 35 CCGGAGGAGCTGTGGC 18

RESULT 3

US-08-795-006A-22/c
Sequence 22, Application US/08795006A
Patent No. 5840579

GENERAL INFORMATION:

APPLICANT: Boeke, Jef
APPLICANT: Brachmann, Rainer
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING P53
TITLE OF INVENTION: MUTATIONS WHICH SUPPRESS P53 CANCER MUTATIONS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSER: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,006A
FILING DATE: 05-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.03170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX:

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-795-006A-22

Query Match 100.0%; Score 18; DB 2; Length 133;

Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGAGCTGTGGC 18
DB 35 CCGGAGGAGCTGTGGC 18

RESULT 4

US-09-184-073-22/c
Sequence 22, Application US/09184073
Patent No. 6183964

GENERAL INFORMATION:

APPLICANT: Boeke, Jef
APPLICANT: Brachmann, Rainer
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING P53
TITLE OF INVENTION: MUTATIONS WHICH SUPPRESS P53 CANCER MUTATIONS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:

ADDRESSER: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,073
FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,006
FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.03170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX:

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-09-184-073-22

Query Match 100.0%; Score 18; DB 3; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGAGCTGTGGC 18
DB 35 CCGGAGGAGCTGTGGC 18

RESULT 5

US-08-472-239-1/c
Sequence 1, Application US/08472239
Patent No. 5728526

GENERAL INFORMATION:

APPLICANT: GEORGE, Jr., Albert L.
APPLICANT: BHATNAGAR, Satish K.
APPLICANT: NAZARENKO, Irena
TITLE OF INVENTION: METHOD FOR ANALYZING A NUCLEOTIDE
TITLE OF INVENTION: SEQUENCE AND KIT THEREFOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: BURNS, DONNE, SWECKER & MATTHIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,239
FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Mukai, Robert G.
REGISTRATION NUMBER: 28,531

REFERENCE/DOCKET NUMBER: 020160-229
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 800 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-472-239-1

Query Match 100.0%; Score 18; DB 1; Length 800;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 108 CCGGAGGCGAGTCTGGC 91

RESULT 6
US-09-414-436-4/c
Sequence 4, Application US/09414436
Patent No. 6294384
GENERAL INFORMATION:
APPLICANT: Dell'Acqua, Giorgio
APPLICANT: Mann, Michael J.
TITLE OF INVENTION: Compositions and Methods Based Upon an Isoform of p53
FILE REFERENCE: p53f
CURRENT APPLICATION NUMBER: US/09/414,436
EARLIER FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: 60/103,849
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1070
TYPE: DNA
ORGANISM: Homo sapiens
US-09-414-436-4

Query Match 100.0%; Score 18; DB 3; Length 1070;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 127 CCGGAGGCGAGTCTGGC 110

RESULT 7
US-08-047-041A-13/c
Sequence 13, Application US/08047041A
Patent No. 5527676
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detection of Loss of the Wild-Type p53
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001-4597
COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,041A
FILING DATE: 22-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446,584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107,42917
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9299
TELEFAX: 202-508-9100
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
MAP POSITION: 17p13.1
PUBLICATION INFORMATION:
AUTHORS: Harris, N.
JOURNAL: Mol. Cell. Biol
VOLUME: 6
ISSUE: 12
PAGES: 4650-4656
DATE: 1986
US-08-047-041A-13

Query Match 100.0%; Score 18; DB 1; Length 1303;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 113 CCGGAGGCGAGTCTGGC 96

RESULT 8
US-08-047-041A-12/c
Sequence 12, Application US/08047041A
Patent No. 5527676
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detection of Loss of the Wild-Type p53
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA

ZIP: 20001.4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047.041A
FILING DATE: 22-MAR-1993
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/928.661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446.584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330.566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42917
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
MAP POSITION: 17p13.1
PUBLICATION INFORMATION:
AUTHORS: Harris, N.
TITLE: Molecular basis for heterogeneity of the
TITLE: human p53 protein
JOURNAL: Mol. Cell. Biol.
VOLUME: 6
ISSUE: 12
PAGES: 4650-4656
DATE: 1986
US-08-047-041A-12

Query Match 100.0%; Score 18; DB 1; Length 1307;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 117 CCGGAGGCGAGTCTGGC 100

RESULT 9
US-07-912-011-1/c
Sequence 1, Application US/07912011
Patent No. 5382510
GENERAL INFORMATION:
APPLICANT: Levine, Arnold J.
APPLICANT: Shenk, Thomas E.
APPLICANT: Finlay, Cathy A.
TITLE OF INVENTION: Probes for Detecting Mutant p53
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSES: Imclone Systems Incorporated
STREET: 180 Varlick Street
CITY: New York

STATE: New York
COUNTRY: USA
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/912.011
FILING DATE: 10-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Felt, Irving N.
REGISTRATION NUMBER: 28,601
REFERENCE/DOCKET NUMBER: LEV-1-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-645-1405
TELEFAX: 212-645-2054
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-07-912-011-1

Query Match 100.0%; Score 18; DB 1; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 127 CCGGAGGCGAGTCTGGC 110

RESULT 10
US-08-347-792-1/c
Sequence 1, Application US/08347792
Patent No. 5573925
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos D.
TITLE OF INVENTION: p53 Proteins With Altered
TITLE OF INVENTION: Tetramerization Domains
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSES: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/347.792
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Maty E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST58USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1314
US-08-347-792-1

Query Match 100.0%; Score 18; DB 1; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGGC 18
|||||
DB 127 CCCGGAAGCAGCTGGC 110

RESULT 11

US-08-431-357-1/c
Sequence 1, Application US/08431357
Patent No. 5721340

GENERAL INFORMATION:
APPLICANT: Halazoneis, Thanos D.
TITLE OF INVENTION: p53 Proteins With Altered
TITLE OF INVENTION: Tetramerization Domains
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/431,357
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/347,792
FILING DATE: 28-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST58USA
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1314
US-08-431-357-1

Query Match 100.0%; Score 18; DB 1; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGGC 18
|||||
DB 127 CCCGGAAGCAGCTGGC 110

RESULT 12
US-08-697-221-1/c
Sequence 1, Application US/08697221
Patent No. 5847083

GENERAL INFORMATION:
APPLICANT: Halazoneis, Thanos D.
TITLE OF INVENTION: Modified p53 Constructs and Uses
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/697,221
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,802
FILING DATE: 22-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kodroff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: WST64AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1314
US-08-697-221-1

Query Match 100.0%; Score 18; DB 2; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGGC 18
|||||
DB 127 CCCGGAAGCAGCTGGC 110

RESULT 13

US-08-392-542-1/c
Sequence 1, Application US/08392542
Patent No. 6169073

GENERAL INFORMATION:
APPLICANT: Halazoneis, Thanos
TITLE OF INVENTION: Peptides and Peptidomimetics with
TITLE OF INVENTION: Structural Similarity to Human p53 That Activate p53
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.

```

;
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/392,542
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske, Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 0486,48439
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 508-9100
; TELEFAX: 202 508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1317 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
;
US-08-392-542-1
;
Query Match 100.0%; Score 18; DB 3; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGGAGGCGAGCTTGGC 18
Db 127 CCGGAGGCGAGCTTGGC 110

RESULT 14
US-08-894-327-1/c
; Sequence 1, Application US/08894327
; Patent No. 6245886
; GENERAL INFORMATION:
; APPLICANT: Halazonec, Thanos
; TITLE OF INVENTION: peptides and peptidomimetics with
; TITLE OF INVENTION: structural similarity to human p53 that activate p53
; TITLE OF INVENTION: function
; FILE REFERENCE: 2973,19998
; CURRENT APPLICATION NUMBER: US/08/894,327
; CURRENT FILING DATE: 1997-12-04
; EARLIER APPLICATION NUMBER: pctus96/01535
; EARLIER FILING DATE: 1996-02-16
; EARLIER APPLICATION NUMBER: 08/392,542
; EARLIER FILING DATE: 1995-02-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1317
; TYPE: DNA
; ORGANISM: Homo sapiens
;
US-08-894-327-1
;
Query Match 100.0%; Score 18; DB 3; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGGAGGCGAGCTTGGC 18
Db 127 CCGGAGGCGAGCTTGGC 110

RESULT 15
US-09-147-751-8/c
```

```

;
; Sequence 8, Application US/09147751
; Patent No. 6335164
; GENERAL INFORMATION:
; APPLICANT: KIGAWA, Koji
; APPLICANT: YANAKA, Mikayo
; APPLICANT: KUSUMI, Kayo
; APPLICANT: MUKAI, Eli
; APPLICANT: OBARA, Kazuaki
; TITLE OF INVENTION: METHODS FOR TARGETING, ENRICHING,
; TITLE OF INVENTION: DETECTING AND/OR ISOLATING TARGET NUCLEIC ACID SEQUENCE
; TITLE OF INVENTION: USING REG- LIKE RECOMBINASE
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSER: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A
; ZIP: 20007-5109
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/147,751
; FILING DATE: 18-MAY-1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/JP97/03019
; FILING DATE: 29-AUG-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8/347090
; FILING DATE: 26-DEC-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 8/229061
; FILING DATE: 29-AUG-1996
; FILING DATE: 29-AUG-1996
; APPLICATION NUMBER: JP 8/229061
; ATTORNEY/AGENT INFORMATION:
; NAME: Maehius, Stephen B.
; REGISTRATION NUMBER: 35,264
; REFERENCE/DOCKET NUMBER: 8435/108
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1317 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
;
US-09-147-751-8
;
Query Match 100.0%; Score 18; DB 4; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGGAGGCGAGCTTGGC 18
Db 127 CCGGAGGCGAGCTTGGC 110

RESULT 16
US-09-305-914-1/c
; Sequence 1, Application US/09305914
; Patent No. 6388062
; GENERAL INFORMATION:
; APPLICANT: Halazonec, Thanos D.
; APPLICANT: Stavridi, Elena S.
; TITLE OF INVENTION: Modified p53 Tetramerization Domains Having Hydrophobic
; TITLE OF INVENTION: Amino Acid Substitutions
; FILE REFERENCE: WST84AUSA
; CURRENT APPLICATION NUMBER: US/09/305,914
```

CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: 60/084,839
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO: 1
LENGTH: 1317
TYPE: DNA
ORGANISM: human p53
FEATURE:
NAME/KEY: CDS
LOCATION: (136)..(1314)
US-09-305-914-1

Query Match 100.0%; Score 18; DB 4; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 127 CCGGAGGCGAGTCTGGC 110

RESULT 17
US-09-685-027-1/c
Sequence 1, Application US/09685027
Patent No. 6420118
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos
Hartwig, Wolfgang
TITLE OF INVENTION: Peptides and Peptidomimetics with
Structural Similarity to Human p53 That Activate p53
Function
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/685,027
FILING DATE: 10-Oct-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/392,542
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 0486,48439
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-685-027-1

Query Match 100.0%; Score 18; DB 4; Length 1317;

Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCGGAGGCGAGTCTGGC 18
DB 127 CCGGAGGCGAGTCTGGC 110

RESULT 18
PCT-US95-15353-1/c
Sequence 1, Application PC/TUS9515353
GENERAL INFORMATION:
APPLICANT: The Wistar Institute of Anatomy
and Biology
APPLICANT: Halazonetis, Thanos D.
TITLE OF INVENTION: p53 Proteins with Altered
TITLE OF INVENTION: Tetramerization Domains
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15353
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/347,792
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/431,357
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/456,623
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST58CPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1314
PCT-US95-15353-1

Query Match 100.0%; Score 18; DB 5; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
DB 127 CCGGAGGCGAGTCTGGC 110

RESULT 19
US-09-404-879A-332

; Sequence 332, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 184
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-404-879A-332

Query Match 85.6%; Score 15.4; DB 4; Length 184;
Best Local Similarity 94.1%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCGAGTCTGGC 18
DB 112 CCGAAGGCGAGTCTGGC 128

RESULT 20
US-09-702-705-1634/C
; Sequence 1634, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1634
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-702-705-1634

Query Match 85.6%; Score 15.4; DB 4; Length 447;
Best Local Similarity 94.1%; Pred. No. 78;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCGAGTCTGGC 18
DB 73 CCGAAGGCGAGTCTGGC 57

RESULT 21
US-09-736-457-1634/C
; Sequence 1634, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aljun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1634
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-736-457-1634

Query Match 85.6%; Score 15.4; DB 4; Length 447;
Best Local Similarity 94.1%; Pred. No. 78;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCGAGTCTGGC 18
DB 73 CCGAAGGCGAGTCTGGC 57

RESULT 22
US-09-614-124B-1634/C
; Sequence 1634, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1634
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-614-124B-1634

Query Match 85.6%; Score 15.4; DB 4; Length 447;
Best Local Similarity 94.1%; Pred. No. 78;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCGAGTCTGGC 18
DB 73 CCGAAGGCGAGTCTGGC 57

RESULT 23
US-09-671-325-1634/C
; Sequence 1634, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom

```

; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1634
; LENGTH: 447
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-671-325-1634
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Query Match      85.6%; Score 15.4; DB 4; Length 447;
Best Local Similarity 94.1%; Pred. No. 78;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      2 CCGAAGGAGCTCTGGC 18
        |||||
Db       73 CCGAAGGAGCTCTGGC 57
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RESULT 24
US-09-385-982-206/C
; Sequence 206, Application US/09385982
; Patent No. 6282314
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDDA-260X
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 206
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(633)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-206
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Query Match      85.6%; Score 15.4; DB 3; Length 633;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      2 CCGAAGGAGCTCTGGC 18
        |||||
Db       426 CCGAAGGAGCTCTGGC 410
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RESULT 25
US-09-222-575-81
; Sequence 81, Application US/09222575
; Patent No. 6387697
; GENERAL INFORMATION:
; APPLICANT: Yugu, Jiang
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
```

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; TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
; FILE REFERENCE: 210121.470
; CURRENT APPLICATION NUMBER: US/09/222,575
; CURRENT FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Human
US-09-222-575-81
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Query Match      85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      2 CCGAAGGAGCTCTGGC 18
        |||||
Db       575 CCGAAGGAGCTCTGGC 591
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Search completed: March 2, 2004, 03:48:42
Job time : 54 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 23:55:06 ; Search time 2529 Seconds
(without alignments)
212.542 Million cell updates/sec

Title: us-09-848-868-35

Perfect score: 18
Sequence: 1 cccggaagcagctcggc 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database :
EST1:
1: em_estba:*
2: em_esthum:*
3: em_estnu:*
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24: em_estfun:*
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26: em_estfun:*
27: em_estfun:*
28: gb_est1:*
29: gb_est2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Match	Length	ID	Description
C 1	18	100.0	190	9	AU076984	AU076984
C 2	18	100.0	203	9	AA296373	AA296373
C 3	18	100.0	230	14	CB117906	CB117906
C 4	18	100.0	234	14	H97230	H97230

C 5	18	100.0	360	12	BG257442	BG257442
C 6	18	100.0	401	10	AM407968	AM407968
C 7	18	100.0	401	10	CB149902	CB149902
C 8	18	100.0	478	14	BM834910	BM834910
C 9	18	100.0	513	9	AU129655	AU129655
C 10	18	100.0	521	10	BT794506	BT794506
C 11	18	100.0	537	14	CB135305	CB135305
C 12	18	100.0	538	12	BM833945	BM833945
C 13	18	100.0	540	14	CB150761	CB150761
C 14	18	100.0	554	9	AU127286	AU127286
C 15	18	100.0	575	9	AU280602	AU280602
C 16	18	100.0	590	12	BM788930	BM788930
C 17	18	100.0	590	12	BM849186	BM849186
C 18	18	100.0	592	12	BM849478	BM849478
C 19	18	100.0	602	12	BM833776	BM833776
C 20	18	100.0	606	12	BM764147	BM764147
C 21	18	100.0	606	12	BM772261	BM772261
C 22	18	100.0	612	14	CB138393	CB138393
C 23	18	100.0	622	10	BM613913	BM613913
C 24	18	100.0	633	9	AU131823	AU131823
C 25	18	100.0	649	14	CB134750	CB134750
C 26	18	100.0	657	12	BM390105	BM390105
C 27	18	100.0	682	12	BM328554	BM328554
C 28	18	100.0	688	9	AU121050	AU121050
C 29	18	100.0	694	9	AU124510	AU124510
C 30	18	100.0	707	12	BM013389	BM013389
C 31	18	100.0	723	9	AU141723	AU141723
C 32	18	100.0	724	9	AU131952	AU131952
C 33	18	100.0	726	12	BM012402	BM012402
C 34	18	100.0	729	9	AU141300	AU141300
C 35	18	100.0	732	12	BM048582	BM048582
C 36	18	100.0	744	18	BE273022	BE273022
C 37	18	100.0	750	12	BM048815	BM048815
C 38	18	100.0	758	12	BT839950	BT839950
C 39	18	100.0	762	13	BM462478	BM462478
C 40	18	100.0	765	12	BM044564	BM044564
C 41	18	100.0	765	12	BM046401	BM046401
C 42	18	100.0	765	12	BM048326	BM048326
C 43	18	100.0	767	12	BM481823	BM481823
C 44	18	100.0	781	9	AU120569	AU120569
C 45	18	100.0	808	12	BT821174	BT821174
C 46	18	100.0	815	12	BT905893	BT905893
C 47	18	100.0	817	13	BU092747	BU092747
C 48	18	100.0	818	13	BM224113	BM224113
C 49	18	100.0	832	13	BM228424	BM228424
C 50	18	100.0	847	9	AU139600	AU139600
C 51	18	100.0	851	9	AL530077	AL530077
C 52	18	100.0	871	12	BM106488	BM106488
C 53	18	100.0	887	13	BM868666	BM868666
C 54	18	100.0	890	13	BU092819	BU092819
C 55	18	100.0	897	13	BM042658	BM042658
C 56	18	100.0	898	13	BU0508407	BU0508407
C 57	18	100.0	905	9	AU130707	AU130707
C 58	18	100.0	905	13	BM059887	BM059887
C 59	18	100.0	907	13	BM229042	BM229042
C 60	18	100.0	913	10	BM032445	BM032445
C 61	18	100.0	916	9	AL520820	AL520820
C 62	18	100.0	917	10	BF342477	BF342477
C 63	18	100.0	923	13	BM019242	BM019242
C 64	18	100.0	924	13	BT1917918	BT1917918
C 65	18	100.0	927	12	BM327832	BM327832
C 66	18	100.0	927	13	BM165476	BM165476
C 67	18	100.0	930	12	BM046196	BM046196
C 68	18	100.0	936	13	BM0894209	BM0894209
C 69	18	100.0	937	13	BM025820	BM025820
C 70	18	100.0	941	18	BT1518429	BT1518429
C 71	18	100.0	949	13	BM0277633	BM0277633
C 72	18	100.0	963	12	BM338735	BM338735
C 73	18	100.0	972	12	BM423840	BM423840
C 74	18	100.0	975	10	BT797075	BT797075
C 75	18	100.0	977	13	BM023115	BM023115
C 76	18	100.0	992	13	BM214218	BM214218
C 77	18	100.0	1005	13	BM0331123	BM0331123

C 78	18	100.0	1060	13	BU157354	AGENCOURT	C 151	15.4	85.6	424	12	B1817349	B1817349 GI-F5 Axi
C 79	18	100.0	1087	12	BG338352	602436132	C 152	15.4	85.6	424	14	W30204	W30204 mc26d10.r1
C 80	18	100.0	1089	12	BM466114	AGENCOURT	C 153	15.4	85.6	427	14	CP116695	CP116695 Shu120m1
C 81	18	100.0	1123	10	BE900862	601673833	C 154	15.4	85.6	428	9	A1909705	A1909705 PM-BT20-
C 82	18	100.0	1201	9	AL530477	AL530477	C 155	15.4	85.6	428	14	R58670	R58670 G4595 Fetal
C 83	18	100.0	1201	13	BX345594	BX345594	C 156	15.4	85.6	436	9	A1759475	A1759475 E15STea28
C 84	18	100.0	1333	12	BM469215	AGENCOURT	C 157	15.4	85.6	439	10	BP117509	BP117509 u237b07.Y
C 85	17.6	97.8	998	9	AL521702	AL521702	C 158	15.4	85.6	440	12	BQ34809	BQ34809 PMO-BN017
C 86	17	94.4	416	9	AA117861	AA117861	C 159	15.4	85.6	452	9	AL036065	AL036065 DKF2P564F
C 87	17	94.4	737	13	AX396796	AX396796	C 160	15.4	85.6	454	13	BY482752	BY482752 BX482752
C 88	17	94.4	1016	13	BX396796	AX396796	C 161	15.4	85.6	465	10	AM885823	AM885823 RC4-OT007
C 89	16.6	92.2	884	29	CNS02160	CNS02160	C 162	15.4	85.6	470	12	BE106945	BE106945 UI-R-BT1-
C 90	16.4	91.1	268	9	AA298090	AA298090	C 163	15.4	85.6	478	10	BC961196	BC961196 PMO-CT082
C 91	16.4	91.1	303	14	R25957	R25957	C 164	15.4	85.6	478	14	CF7990074	CF7990074 867418 MA
C 92	16.4	91.1	372	10	BF651887	BF651887	C 165	15.4	85.6	478	14	HO3678	HO3678 YJ42B11.r1
C 93	16.4	91.1	498	14	H50566	H50566	C 166	15.4	85.6	480	14	W49749	W49749 ZC41608.r1
C 94	16.4	91.1	513	10	BF043070	BF043070	C 167	15.4	85.6	483	10	AM630245	AM630245 hb8d07.Y
C 95	16.4	91.1	604	10	BF541984	BF541984	C 168	15.4	85.6	484	9	AA967116	AA967116 ua40e05.r
C 96	16.4	91.1	644	10	BE144316	BE144316	C 169	15.4	85.6	485	12	BU061083	BU061083 BU061083
C 97	16.4	91.1	685	12	BG432786	BG432786	C 170	15.4	85.6	487	13	BQ319870	BQ319870 PMO-CT082
C 98	16.4	91.1	697	12	BG294801	BG294801	C 171	15.4	85.6	485	10	AM885788	AM885788 RC4-OT007
C 99	16.4	91.1	723	12	BG621970	BG621970	C 172	15.4	85.6	487	9	AA111707	AA111707 mp60a11.r
C 100	16.4	91.1	740	9	BU139631	BU139631	C 173	15.4	85.6	497	10	BE106377	BE106377 UI-R-BT1-
C 101	16.4	91.1	790	12	BG212909	BG212909	C 174	15.4	85.6	503	10	BE567951	BE567951 UI-R-B00-
C 102	16.4	91.1	815	9	BU119797	BU119797	C 175	15.4	85.6	504	10	BE833812	BE833812 RC4-OT007
C 103	16.4	91.1	837	9	BU119797	BU119797	C 176	15.4	85.6	505	14	CF569008	CF569008 017-102-r
C 104	16.4	91.1	844	10	BF316085	BF316085	C 177	15.4	85.6	506	9	AA009423	AA009423 zeb2c08.r
C 105	16.4	91.1	856	13	BU146860	AGENCOURT	C 178	15.4	85.6	506	14	CB723596	CB723596 UI-M-GK0-
C 106	16.4	91.1	861	9	BU118353	BU118353	C 179	15.4	85.6	509	10	AM673601	AM673601 ba5b01.Y
C 107	16.4	91.1	876	12	BG435676	602506969	C 180	15.4	85.6	510	10	AM520875	AM520875 UI-R-B0P
C 108	16.4	91.1	916	13	BQ919531	BQ919531	C 181	15.4	85.6	510	14	CB143418	CB143418 K-EST0197
C 109	16.4	91.1	931	12	B114676	602861893	C 182	15.4	85.6	511	12	B1817644	B1817644 G2-M6 Axi
C 110	16.4	91.1	942	9	BU117581	BU117581	C 183	15.4	85.6	514	9	AA184937	AA184937 mc88a02.r
C 111	16.4	91.1	1014	12	BG598893	602703310	C 184	15.4	85.6	515	12	B1775888	B1775888 468609 MA
C 112	16.4	91.1	1038	10	BE786919	BE786919	C 185	15.4	85.6	518	28	AA296219	AA296219 PRC1-23-1
C 113	16.4	91.1	1040	12	BM644765	BM644765	C 186	15.4	85.6	521	10	AM836191	AM836191 QY2-LT005
C 114	16.4	91.1	1040	13	BQ436739	AGENCOURT	C 187	15.4	85.6	524	12	B1817305	B1817305 GI-D10 AX
C 115	16.4	91.1	1170	12	BM013221	600634947	C 188	15.4	85.6	530	12	BM721923	BM721923 UI-E-B00-
C 116	16.4	91.1	1170	12	BM013221	600634947	C 189	15.4	85.6	539	14	CB265876	CB265876 1004781 H
C 117	16	88.9	760	9	BF036211	DKF2P564H	C 190	15.4	85.6	540	12	BG537072	BG537072 60265158
C 118	16	88.9	978	10	BF036211	BF036211	C 191	15.4	85.6	545	9	AA177319	AA177319 EST220936
C 119	16	88.9	1201	13	EX355038	EX355038	C 192	15.4	85.6	550	9	AA277412	AA277412 vb69d11.r
C 120	15.4	85.6	105	10	AM388465	AM388465	C 193	15.4	85.6	555	10	BG643376	BG643376 v67a06.Y
C 121	15.4	85.6	220	9	AV019229	AV019229	C 194	15.4	85.6	556	10	AM388278	AM388278 MR2-ST012
C 122	15.4	85.6	244	9	AA331081	EST34946	C 195	15.4	85.6	559	29	CC753990	CC753990 ZMBB013
C 123	15.4	85.6	250	14	CB029906	TGEBTzyd1	C 196	15.4	85.6	562	14	CB266565	CB266565 1005471 H
C 124	15.4	85.6	269	9	AA360662	AA360662	C 197	15.4	85.6	564	9	AU280282	AU280282 AU280282
C 125	15.4	85.6	273	9	AA330252	EST33954	C 198	15.4	85.6	570	12	BG530001	BG530001 602558845
C 126	15.4	85.6	273	10	AM336780	AM336780	C 199	15.4	85.6	571	13	B0126161	B0126161 1114a07.Y
C 127	15.4	85.6	287	9	AA333978	EST36122	C 200	15.4	85.6	571	28	AA109510	AA109510 PRC1-23-4
C 128	15.4	85.6	292	12	B1015695	B1015695							
C 129	15.4	85.6	296	9	AI933573	AI933573							
C 130	15.4	85.6	299	9	AA328516	BY354672							
C 131	15.4	85.6	300	13	BY354672	BY354672							
C 132	15.4	85.6	324	9	AA358056	AA358056							
C 133	15.4	85.6	325	12	BG608755	BG608755							
C 134	15.4	85.6	361	14	CB270401	CB270401							
C 135	15.4	85.6	363	12	B1295366	B1295366							
C 136	15.4	85.6	375	14	R25637	R25637							
C 137	15.4	85.6	376	29	CG781817	CG781817							
C 138	15.4	85.6	386	10	BF706710	BF706710							
C 139	15.4	85.6	391	12	BG814972	dab98c10							
C 140	15.4	85.6	394	29	CG344533	CG344533							
C 141	15.4	85.6	395	29	CB776194	AMGNDC:S							
C 142	15.4	85.6	399	29	CG782144	CG782144							
C 143	15.4	85.6	401	29	CG773386	CG773386							
C 144	15.4	85.6	402	29	CG782158	CG782158							
C 145	15.4	85.6	404	13	C28802	C28802							
C 146	15.4	85.6	409	10	BB680161	BB680161							
C 147	15.4	85.6	409	12	BM462266	BM462266							
C 148	15.4	85.6	409	28	AQ006068	CIT-HSP-2							
C 149	15.4	85.6	413	12	BM106200	BM106200							
C 150	15.4	85.6	420	9	AA329660	EST33298							

ALIGNMENTS

RESULT 1

LOCUS

DEFINITION

KEYWORDS

ACCESSION

VERSION

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

AU076984/c
 AU076984 Sugano cDNA library Homo sapiens cDNA clone kata4737
 similar to 5'-end region of Human p53 cellular tumor antigen mRNA,
 mRNA sequence.

AU076984.1 GI:7439546
 Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 190)
 Suzuki,T., Ishihara,D., Sasaki,M., Nakagawa,H., Hata,H.,
 Tsumoda,T., Watanabe,M., Komatsu,T., Ota,T., Isegaki,T., Suyama,A.
 and Sugano,S.

Statistical analysis of the 5' untranslated region of human mRNA

JOURNAL
Genomics 64 (3), 286-297 (2000)
MEDLINE
20221373
PubMed
10756096
COMMENT

using 'Oligo-Capped' cDNA libraries
Department of Medical Science, University of Tokyo
Institute of Medical Science, University of Tokyo
4-6-1, Shirokanedai, Minatoku, Tokyo 108-8639, Japan
Email: yasukik@ims.u-tokyo.ac.jp
Suzuki, Y., Yoshitomo-Nakagawa, K., Maruyama, K., Suyama, A. and
Sugano, S. Construction and characterization of a full
length-enriched and a 5'-end-enriched cDNA library. Gene 200 (1-2),
149-156 (1997)
This clone was obtained from a 'full length-enriched' cDNA library
constructed by 'Oligo-Capping' method. The coding region starts
from the 50 bp upstream to the 3'-end.
Location/Qualifiers
1..190
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="Ka14737"
/clone_lib="Sugano cDNA library"

ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 190;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAAGGCGAGCTGTGGC 18
|||||
Db 132 CCGGAAGGCGAGCTGTGGC 115

RESULT 2
AA296373 203 bp mRNA linear EST 18-APR-1997
LOCUS
DEFINITION
EST10934 umbilical vein endothelial cells II Homo sapiens cDNA 5'
end similar to transformation-associated protein p53, mRNA
sequence.

ACCESSION
AA296373
VERSION
AA296373.1 GI:1948779
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 203)
Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man, M., C.,
Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D.,
Fitzgerald, L.M., Fritch, W.M., Fritchman, J.L., Georghiou, N.S.,
Glodek, A., Gresh, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr.,
Keller, J.M., Kelley, J.C., Liu, L.-I., Marmaro, S.M., Merrick, J.M.,
Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shirley, R.,
Small, K.V., Sprague, T.A., Uterback, T.R., Weidman, J.F., Li, Y.,
Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinke, D., Feng, D.-P., Ferris, A., Fischer, C., Hastings, G.A.,
He, W.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K.,
Kozak, D.L., Kusch, C., Hung, J., Li, H., Welsner, P.S., Olsen, H.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Dillon, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C.,
Fraser, C.M., and Venter, J.C.

TITLE
JOURNAL
MEDLINE
PUBMED
9602680
COMMENT

Other ESTs: THC168370
Contact: Kerlavage, AR
Bioinformatics

The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlavage@igr.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
Seq primer: M3 Reverse.
Location/Qualifiers
1..203
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="ATCC (insect):194290"
/db_xref="taxon:9606"
/cell_type="endothelial cell"
/dev_stage="fetus"
/clone_lib="Umbilical vein endothelial cells II"
/note="Organ: umbilical vein; Vector: pBluescript SK-";
Site_1: EcoRI; Site_2: XhoI"

FEATURES

Query Match 100.0%; Score 18; DB 9; Length 203;
Best Local Similarity 100.0%; Pred. No. 4.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAAGGCGAGCTGTGGC 18
|||||
Db 118 CCGGAAGGCGAGCTGTGGC 101

RESULT 3
CB117906 230 bp mRNA linear EST 28-JAN-2003
LOCUS
DEFINITION
K-EST0163962 B1T694954 Homo sapiens cDNA clone B1T694954-4-F11 5',
mRNA sequence.
ACCESSION
CB117906
VERSION
CB117906.1 GI:27943713
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM

REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 230)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.

TITLE
JOURNAL
COMMENT
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boseon-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 row: F column: 11
High quality sequence frop: 230.
Location/Qualifiers
1..230
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="B1T694954-4-F11"
/sex="M"
/lab_host="Top10F"
/clone_lib="B1T694954"
/note="Organ: Brain; Vector: PCNS-D2; Site 1: EcoRI;
Site 2: NotI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first

FEATURES

strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for electroporation of competent cells E. coli Top10⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 14; Length 230;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 CCGGAGGAGGAGCTGGC 18
134 CCGGAGGAGGAGCTGGC 117

DB

RESULT 4
H97230/c 234 bp mRNA linear EST 11-DEC-1995
DEFINITION YX04912.t1 Soares melanocyte 2NDHM Homo sapiens cDNA clone
IMAGE:260806 5' similar to gb:XE4156_rnal CELLULAR TUMOR ANTIGEN
P53 (HUMAN) mRNA sequence.

ACCESSION H97230.1 GI:1114273

VERSION H97230.1

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 234)
Hillier, L., Clark, N., Dubuque, T., Eilston, K., Hawkins, M.,
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marra, M.,
Parsons, J., Rifkin, L., Rohlfing, T., Soares, M., Tan, F.,
Trevaskis, E., Waterston, R., Williamson, A., Wohlmann, P. and
Wilson, R.

REFERENCE

AUTHORS

TITLE The Washu-Merck EST Project
JOURNAL Unpublished (1995)
COMMENT Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu

High quality sequence starts: 1
High quality sequence stops: 1
Source: IMAGE Consortium, LNL
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Trace considered overall poor quality
Insert Length: 2246 Std Error: 0.00
Seq primer: M13RPI
High quality sequence stop: 1.
Location/Qualifiers

FEATURES

source

1..234
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:3870448"
/db_xref="taxon:9606"
/clone="IMAGE:260806"
/sex="Male"
/tissue_type="melanocyte"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares melanocyte 2NDHM"
/note="Vector: pT73D (Pharmacia) with a modified
polylinker. Site 1: Not I; Site 2: Eco RI; 1st strand cDNA
was primed with a Not I - Oligo(dT) primer [5'
TGTTCACATCTGAAGTGGAGCGCGCTTTTCTTTTCTTTT 3']
double-stranded cDNA was size selected, ligated to Eco RI

adapters (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of a modified pT73 vector
(Pharmacia). Library constructed by Bento Soares and
M. Fatima Bonaldo. RNA from normal foreskin melanocytes
(FS374) was kindly provided by Dr. Anthony P. Albino."

ORIGIN

Query Match 100.0%; Score 18; DB 14; Length 234;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 CCGGAGGAGGAGCTGGC 18
104 CCGGAGGAGGAGCTGGC 87

DB

RESULT 5
BG257442/c 360 bp mRNA linear EST 13-FEB-2001
DEFINITION 602377775F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4508539 5',
mRNA sequence.

ACCESSION BG257442.1 GI:12767258

VERSION BG257442

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 360)
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNL0387 row: e column: 20
High quality sequence stop: 360.
Location/Qualifiers

FEATURES

source

1..360
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4508539"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-Sport6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 360;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 CCGGAGGAGGAGCTGGC 18
107 CCGGAGGAGGAGCTGGC 90

DB

RESULT 6
AM407968/c 401 bp mRNA linear EST 16-FEB-2000
LOCUS AM407968
DEFINITION UI-HF-BX0-ad1-a-03-0-UI.r2 NIH_MGC_38 Homo sapiens cDNA clone
IMAGE:3061901 5', mRNA sequence.

ACCESSION AM407368
 VERSION AM407368.1 GI:6927025
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 401)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LMNL at:
www.bio.lmnl.gov/bdnp/image/image.html
 Seq primer: M13 Forward

FEATURES

Source

Location/Qualifiers
 1..401
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3061901"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_id="NIH MGC 38"
 /note="Vector: pTZ19-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (2.5-3.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fátima
 Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 100.0%; Score 18; DB 10; Length 401;
 Best Local Similarity 100.0%; Pred. No. 5e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAAAGCAGCTGGC 18
 |||||
 DB 55 CCGGAAAGCAGCTGGC 38

RESULT 7
 CBI49902/c CBI49902 434 bp mRNA linear EST 29-JAN-2003
 LOCUS K-EST0206507 L15CKX1 Homo sapiens cDNA clone L15CKX1-48-G06 5',
 DEFINITION mRNA sequence.
 ACCESSION CBI49902
 VERSION CBI49902
 KEYWORDS EST.
 SOURCE EST. CBI49902.1 GI:28132859
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 434)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 CONTACT: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409

TITLE

JOURNAL COMMENT

Email: yongsung@mail.kribb.re.kr
 Plate: 48 row: G column: 06
 High quality sequence stop: 434.
 Location/Qualifiers
 1..434

FEATURES

Source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="L15CKX1-48-G06"
 /sex="M"
 /cell_line="CK-K1"
 /lab_host="Top10F"
 /clone_id="L15CKX1"
 /note="Organ: liver; Vector: pCNS-D2; Site 1: EcoRI;
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with
 bacterial alkaline phosphatase (BAP) and then deacapped
 with tobacco acid pyrophosphatase (TAP). The deacapped
 intact mRNA was ligated with DNA-RNA linker including
 EcoRI site by treatment of T4 RNA ligase and the first
 strand cDNA was synthesized from oligo dt-selected mRNA by
 priming with dt-tailed vector. The dt-tailed vector was
 adjusted to have about 60nt. The cDNA vector was
 circularized with E. coli DNA ligase after digestion of
 EcoRI which site is also included in vector. An RNA strand
 converted to a DNA strand by Okayama-Berg method. The
 obtained cDNA vectors were used for transformation of
 competent cells E. coli Top10F by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 14; Length 434;
 Best Local Similarity 100.0%; Pred. No. 5.1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAAAGCAGCTGGC 18
 |||||
 DB 131 CCGGAAAGCAGCTGGC 114

RESULT 8
 LOCUS BM834910/c BM834910 478 bp mRNA linear EST 06-MAR-2002
 DEFINITION K-EST0110069 S11SNV1 Homo sapiens cDNA clone S11SNV1-51-E01 5',
 mRNA sequence.
 ACCESSION BM834910
 VERSION BM834910
 KEYWORDS EST.
 SOURCE EST. BM834910.1 GI:19191319
 ORGANISM Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 478)
 AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
 Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
 Kim,Y.S.
 21C Frontier Korean EST Project 2001
 Unpublished (2002)
 CONTACT: Kim YS
 Genome Research Center
 Korea Research Institute of Bioscience & Biotechnology
 52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
 Tel: +82-42-860-4470
 Fax: +82-42-860-4409
 Email: yongsung@mail.kribb.re.kr
 Plate: 51 row: E column: 01
 High quality sequence stop: 478.
 Location/Qualifiers
 1..478

FEATURES

Source

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="S11SNV1-51-E01"

```

/sex="M"
/tissue_type="Stomach"
/cell_type="Lymphoblast-like"
/cell_line="SNV-1"
/lab_host="TOP10F"
/clone_lib="S11SNV1"
/notes="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI;
Site 2: XhoI; The poly (A)+ RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including SfiI
site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized with Superscript II using SfiI
oligo-dT primer. After first strand synthesis, RNA was
degraded by NaOH treatment and cDNA was amplified by PCR
reaction. The PCR products were digested with SfiI and
cloned into DraIII-digested pME18S-FL3 vector. The
obtained cDNA vectors were used for transformation of
competent cells E. coli TOP10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

```

ORIGIN

```

Query Match      100.0%; Score 18; DB 12; Length 478;
Best Local Similarity 100.0%; Pred. No. 5.3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  CCGGAGGCGAGCTGTGCG 18
         |||
Db       132 CCGGAGGCGAGCTGTGCG 115

```

```

RESULT 9
AUI29655/c      513 bp      mRNA      linear      EST 01-AUG-2002
LOCUS           AUI29655 NT2RP2 Homo sapiens cDNA clone NT2RP205982 5', mRNA
DEFINITION      sequence.
ACCESSION       AUI29655
VERSION         AUI29655.1 GI:10990009
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE       1 (bases 1 to 513)
AUTHORS         Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,T., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE           HRI human cDNA project
JOURNAL         Unpublished (2000)
COMMENT         Contact: Takao Isogai
                  Genomics Laboratory
                  Helix Research Institute
                  1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
                  Tel: 81-438-52-3975
                  Fax: 81-438-52-3986
                  Email: genomics@hri.co.jp
                  HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
                  Research Institute; cDNA library construction; Department of
                  Virology, Institute of Medical Science, University of Tokyo, and
                  Helix Research Institute.

```

FEATURES

```

source          1..513
                  Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP205982"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2RP2"
/notes="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"

```

ORIGIN

```

Query Match      100.0%; Score 18; DB 9; Length 513;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  CCGGAGGCGAGCTGTGCG 18
         |||
Db       184 CCGGAGGCGAGCTGTGCG 167

```

```

RESULT 10
BF794506/c      521 bp      mRNA      linear      EST 12-JAN-2001
LOCUS           BF794506 NT1H_MGC_85 Homo sapiens cDNA clone IMAGE:4339142 5',
DEFINITION      mRNA sequence.
ACCESSION       BF794506
VERSION         BF794506.1 GI:12099560
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE       1 (bases 1 to 521)
AUTHORS         NIH-MGC http://mgc.nci.nih.gov/.
TITLE           National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL         Unpublished (1999)
COMMENT         Contact: Robert Strausberg, Ph.D.
                  Email: gcaps-remail.nih.gov
                  Tissue Procurement: Louis Staudt, M.D., Ph.D.
                  cDNA Library Preparation: Life Technologies, Inc.
                  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
                  DNA Sequencing by: Incyte Genomics, Inc.
                  Clone distribution: MGC clone distribution information can be
                  found through the I.M.A.G.E. Consortium/LNL at:
                  http://image.llnl.gov
                  Plate: LLM9949 row: c column: 15
                  High quality sequence stop: 519.

```

FEATURES

```

source          1..521
                  Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4339142"
/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 85"
/notes="Organ: lymph; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC library."

```

ORIGIN

```

Query Match      100.0%; Score 18; DB 10; Length 521;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1  CCGGAGGCGAGCTGTGCG 18
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Db       163 CCGGAGGCGAGCTGTGCG 146

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RESULT 11
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LOCUS           CB135305 K-EST0187411 LSHLKI Homo sapiens cDNA clone LSHLKI-32-F04 5', mRNA
DEFINITION      sequence.
ACCESSION       CB135305
VERSION         CB135305.1 GI:28102030
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

ORIGIN

REFERENCE

Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 537)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.krribb.re.kr
Plate: 32 row: F column: 04
High quality sequence stop: 537.
Location/Qualifiers

FEATURES

SOURCE

1. 537
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LSHLK1-32-F04"
/sex="M"
/cell_line="HLK-1"
/lab_host="Top10F"
/clone_1b="LSHLK1"
/note="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI;
Site 2: NotI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including
EcoRI site by treatment of T4 RNA ligase and the first
strand cDNA was synthesized from oligo dt-selected mRNA by
priming with dt-tailed vector. The dt-tailed vector was
adjusted to have about 60nt. The cDNA vector was
circularized with E. coli DNA ligase after digestion of
EcoRI which site is also included in vector. An RNA strand
converted to a DNA strand by Okayama-Berg method. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 14; Length 537;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGGAGGAGGAGCTGGC 18
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Db 132 CCGGAGGAGGAGCTGGC 115

RESULT 12
BM833945/c 538 bp mRNA linear EST 06-MAR-2002
LOCUS K-EST010801 S11SNUI Homo sapiens cDNA clone S11SNUI-59-A11 5',
DEFINITION mRNA sequence.
ACCESSION BM833945
VERSION BM833945.1 GI:19190354
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 538)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center

Korea Research Institute of Bioscience & Biotechnology
52 Eeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.krribb.re.kr
Plate: 59 row: A column: 11
High quality sequence stop: 538.
Location/Qualifiers

FEATURES

SOURCE

1. 538
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/clone="S11SNUI-59-A11"
/sex="M"
/tissue_type="Stomach"
/cell_type="Lymphoblast-like"
/cell_line="SKO-1"
/lab_host="Top10F"
/clone_1b="S11SNUI"
/note="Organ: Stomach; Vector: pME18-FL3; Site 1: XhoI;
Site 2: XhoI; The poly (A) + RNA was dephosphorylated with
bacterial alkaline phosphatase (BAP) and then decapped
with tobacco acid pyrophosphatase (TAP). The decapped
intact mRNA was ligated with DNA-RNA linker including SfiI
site by treatment of T4 RNA ligase and the first strand
cDNA was synthesized with Superscript II using SfiI
oligo-dt primer. After first strand synthesis, RNA was
degraded by NaOH treatment and cDNA was amplified by PCR
reaction. The PCR products were digested with SfiI and
cloned into DraIII-digested pYES2-FL3 vector. The
obtained cDNA vectors were used for transformation of
competent cells E. coli Top10F by electroporation method.
The cDNA libraries constructed by this method are
full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 538;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCGGAGGAGGAGCTGGC 18
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Db 152 CCGGAGGAGGAGCTGGC 135

RESULT 13
CB150761/c 540 bp mRNA linear EST 29-JAN-2003
LOCUS K-EST020757 C15NUI7 Homo sapiens cDNA clone C15NUI7-34-H06 5',
DEFINITION mRNA sequence.
ACCESSION CB150761
VERSION CB150761.1 GI:28134341
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 540)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.krribb.re.kr
Plate: 34 row: H column: 06
High quality sequence stop: 540.
Location/Qualifiers

FEATURES

source

1. .540

/organism="Homo sapiens"

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/db_xref="taxon:9606"

/clone_id="C15N017-34-H06"

/sex="F"

/tissue_type="uterine"

/cell_type="epithelial"

/cell_line="SNU-17"

/lab_host="top10f"

/clone_id="C15N017"

/note="Organ: Cervix; Vector: PCNS-D2; Site:1: EcoRI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by printing with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli top10f, by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 14; Length 540;

Best Local Similarity 100.0%; Pred. No. 5.4e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18

DB 133 CCGGAGGCGAGTCTGGC 116

RESULT 14

AU127286/c 554 bp mRNA linear EST 01-AUG-2002

LOCUS AU127286 NT2RP2 Homo sapiens cDNA clone NT2RP2000945 5', mRNA

DEFINITION sequence.

ACCESSION AU127286

VERSION AU127286.1 GI:10952002

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 554)

1 Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Salto,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.

TITLE HRI human cDNA project

JOURNAL Unpublished (2000)

COMMENT Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES

Location/Qualifiers

1. .554

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="NT2RP2000945"

/cell_type="teratocarcinoma"

/cell_line="NT2"

/clone_id="NT2RP2"

/note="Vector: PME18SFL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"

ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 554;

Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18

DB 132 CCGGAGGCGAGTCTGGC 115

RESULT 15

AU280602/c 575 bp mRNA linear EST 31-JUL-2003

LOCUS AU280602 N18SE2 Homo sapiens cDNA clone N18SE2002780 5', mRNA

DEFINITION sequence.

ACCESSION AU280602

VERSION AU280602.1 GI:28299829

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 575)

1 Imabayashi,H., Morii,T., Gojo,S., Kiyono,T., Sugiyama,T., Irie,R., Iseawa,A., Fukuma,M., Kusakari,S., Hata,J., Ishii,S., Yamamoto,J., Isono,Y., Salto,K., Nakamura,Y., Masuno,Y., Nagai,K., Isogai,T., Isogai,T., Hata,J., Tomoya,Y. and Umezawa,A.

TITLE Redifferentiation of dedifferentiated chondrocytes and chondrogenesis of human bone marrow stromal cells via chondrosphere formation with expression profiling by large-scale cDNA analysis

JOURNAL Exp. Cell Res. 288 (1), 35-50 (2003)

MEDLINE 22760698

PUBMED 12878157

COMMENT Contact: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human cDNA project; Sugiyama,T., Wakamatsu,A.; Irie,R.; Umezawa,A.; Fukuma,M.; Kusakari,S.; Hata,J.; Ishii,S.; Yamamoto,J.; Isono,Y.; Salto,K.; Nakamura,Y.; Masuno,Y.; Nagai,K.; Isogai,T.

TITLE HRI human cDNA project; cDNA library construction & 5'-end one pass sequencing: Helix Research Institute.

FEATURES

Location/Qualifiers

1. .575

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="N18SE2002780"

/cell_type="mesenchymal stem cells"

/clone_id="N18SE2"

/note="Vector: PME18SFL3"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 5.5e+02;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18

DB 132 CCGGAGGCGAGTCTGGC 115

RESULT 16

BM788590 590 bp mRNA linear EST 05-MAR-2002

LOCUS BM788590/c

DEFINITION K-EST0067764 S11SNU1 Homo sapiens cDNA clone S11SNU1-24-c03 5',

RNA sequence.
ACCESSION BM788590 GI:19136822
VERSION BM788590.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 590)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 24 row: G column: 03
High quality sequence stop: 590.
Location/Qualifiers
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1..590
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/sex="M"
/tissue_type="Stomach"
/cell_line="Lymphoblast-like"
/lab_host="SNU-1"
/lab_host="Top10F"
/clone_lib="S11SM01"
/note="Origin: Stomach; Vector: pME18-F13; Site 1: XhoI; Site 2: XhoI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII-digested pME18S-F13 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

Query Match 100.0%; Score 18; DB 12; Length 590;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCGGAAGGCGACTGTGCG 18
DB 131 CCCGGAAGGCGACTGTGCG 114

RESULT 17
LOCUS BM849186 590 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0129212 S13KMS5 Homo sapiens cDNA clone S13KMS5-66-B06 5',
RNA sequence.
ACCESSION BM849186
VERSION BM849186.1 GI:19205585
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 590)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 66 row: E column: 06
High quality sequence stop: 590.
Location/Qualifiers
source
1..590
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/clone="S13KMS5-66-B06"
/tissue_type="myeloma"
/cell_line="KMS-5"
/lab_host="Top10F"
/clone_lib="S13KMS5"
/note="Vector: PCNS; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

Query Match 100.0%; Score 18; DB 12; Length 590;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CCCGGAAGGCGACTGTGCG 18
DB 132 CCCGGAAGGCGACTGTGCG 115

RESULT 18
LOCUS BM849478 592 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0129549 S13KMS5 Homo sapiens cDNA clone S13KMS5-69-A07 5',
RNA sequence.
ACCESSION BM849478
VERSION BM849478.1 GI:19205877
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 592)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology

52 Eooun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 69 row: A column: 07
High quality sequence stop: 592.
Location/Qualifiers
1..592

FEATURES

/organism="Homo sapiens"
/mol_type="mRNA"
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/cell_line="KMS-5"
/lab_host="Top10F"
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/note="Vector: pCNS; Site_1: EcoRI; Site_2: NotI. The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 592;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGCTGTGCG 18
|||||
DB 133 CCGGAGGCGAGCTGTGCG 115

RESULT 19

BM833776/c 602 bp mRNA linear EST 06-MAR-2002
LOCUS BM833776
DEFINITION K-EST0108618 S13SNUI Homo sapiens cDNA clone S13SNUI-57-B08 5',
mRNA sequence.
ACCESSION BM833776
VERSION BM833776.1 GI:19190185
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 602)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eooun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 57 row: B column: 08
High quality sequence stop: 602.
Location/Qualifiers
1..602
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TITLE

JOURNAL

COMMENT

FEATURES

source

/mol_type="mRNA"
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/clone_lib="S13SNUI"
/note="Stomach; Vector: pME18-FL3; Site_1: XhoI; Site_2: XhoI. The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII-digested pME18-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 602;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGCTGTGCG 18
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DB 134 CCGGAGGCGAGCTGTGCG 117

RESULT 20

BM764147/c 606 bp mRNA linear EST 04-MAR-2002
LOCUS BM764147
DEFINITION K-EST0045606 S13KMS5 Homo sapiens cDNA clone S13KMS5-23-E10 5',
mRNA sequence.
ACCESSION BM764147
VERSION BM764147.1 GI:19093762
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 606)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eooun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 23 row: E column: 10
High quality sequence stop: 606.
Location/Qualifiers
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/cell_line="KMS-5"
/lab_host="Top10F"
/clone_lib="S13KMS5"
/note="Vector: pCNS; Site_1: EcoRI; Site_2: NotI. The poly

TITLE

JOURNAL

COMMENT

FEATURES

source

(A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 606;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CCCGAGGCGAGCTGGC 18
|||
Db 132 CCCGAGGCGAGCTGGC 115

RESULT 21
BM772261 606 bp mRNA linear EST 04-MAR-2002
LOCUS K-EST0056378 S13XMS581 Homo sapiens cDNA clone S13XMS581-1-B04 5',
DEFINITION mRNA sequence.
ACCESSION BM772261
VERSION BM772261.1 GI:19101876
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 606)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001

TITLE Unpublished (2002)
JOURNAL
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 1 row: B column: 04
High quality sequence stop: 606.
Location/Qualifiers
1. 606

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S13XMS581-1-B04"
/tissue_type="myeloma"
/cell_line="RMS-5"
/lab_host="Top10⁺"
/clone_lib="S13XMS581"
/note="Vector: pCNS.1: EcoRI, Site.2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is

also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promoter as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original library and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the substracted cDNA libraries were constructed by transformation of the remaining DNA into competent cells E. coli Top10⁺ with electroporation method."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 606;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CCCGAGGCGAGCTGGC 18
|||
Db 132 CCCGAGGCGAGCTGGC 115

RESULT 22
CB138393/c 612 bp mRNA linear EST 29-JAN-2003
LOCUS K-EST0191254 U15CKK1 Homo sapiens cDNA clone U15CKK1-29-B07 5',
DEFINITION mRNA sequence.
ACCESSION CB138393
VERSION CB138393.1 GI:2810037
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE

AUTHORS

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 612)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
21C Frontier Korean EST Project 2001

TITLE Unpublished (2002)
JOURNAL
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 29 row: B column: 07
High quality sequence stop: 612.
Location/Qualifiers
1. 612

FEATURES

source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="U15CKK1-29-B07"
/sex="M"
/cell_line="CK-K1"
/lab_host="Top10⁺"
/clone_lib="U15CKK1"
/note="Organ: Liver; Vector: pCNS-D2; Site.1: EcoRI; Site.2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by

priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10⁺ by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 14; Length 612;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGACGAGTCTGGC 18
DB 137 CCGGAGGACGAGTCTGGC 120

RESULT 23 BE613913/c 622 bp mRNA linear EST 20-OCT-2000
LOCUS 601504033F1 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:3905577 5',
DEFINITION mRNA Sequence.

ACCESSION BE613913
VERSION BE613913.1 GI:3895510
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 622)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov

Plate: LMA9713 row: b column: 10
High quality sequence stop: 610.

FEATURES

source

1..622
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="3905577"
/issue_type="telomoyosarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 71"
/note="Organ: uterus; Vector: PCMV-SPORT6; Site 1: Notif; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb."

ORIGIN

Query Match 100.0%; Score 18; DB 10; Length 622;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGACGAGTCTGGC 18
DB 96 CCGGAGGACGAGTCTGGC 79

RESULT 24 AUI31823/c 633 bp mRNA linear EST 01-AUG-2002
LOCUS AUI31823

DEFINITION AUI31823 NT2RNP3 Homo sapiens cDNA clone NT2RNP3003309 5', mRNA sequence.

ACCESSION AUI31823
VERSION AUI31823.1 GI:10992177
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 633)
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saio, K., Kawai, Y., Yamamoto, J., Makatsutsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isega, T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isega
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp

HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
Location/Qualifiers
1..633
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RNP3003309"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2RNP3"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"

FEATURES

source

1..633
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RNP3003309"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2RNP3"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA) induction"

ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 633;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGACGAGTCTGGC 18
DB 130 CCGGAGGACGAGTCTGGC 113

RESULT 25

CB134750/c 649 bp mRNA linear EST 29-JAN-2003
LOCUS K-EST186263 LSHUK1 Homo sapiens cDNA clone LSHUK1-31-F08 5', mRNA
DEFINITION sequence.

ACCESSION CB134750
VERSION CB134750.1 GI:28101108
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 649)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE K-EST186263 LSHUK1 Homo sapiens cDNA clone LSHUK1-31-F08 5', mRNA
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eosun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongseung@mail.kribb.re.kr

Plate: 31 row: F column: 08
High quality sequence stop: 649.

FEATURES

Location/Qualifiers
1. 649

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="LSHLK1-31-F08"
/sex="M"

/cell_line="HLK-1"
/lab_host="Top10F"
/clone_id="LSHLK1"

/note="Organ: Liver; Vector: pCNS-D2; Site 1: EcoRI; Site 2: NotI; The poly (A) + RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then deapped with tobacco acid pyrophosphatase (TAP). The deapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transforation of competent cells E. coli Top10F by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 100.0%; Score 18; DB 14; Length 649;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CCCGAAGGCGAGTCTGGC 18
134 CCCGAAGGCGAGTCTGGC 117

RESULT 26

BG390105/c

LOCUS

602415946F1 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:4524419 5',

DEFINITION

mRNA sequence.

ACCESSION

BG390105

VERSION

BG390105.1 GI:13283651

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 657)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

EMAIL

cgagbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

Plate: LRAM10428 row: k column: 12

High quality sequence stop: 652.

Location/Qualifiers

1. 657

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:4524419"

/tissue_type="embryonal carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 2.5 Kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 657;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CCCGAAGGCGAGTCTGGC 18
119 CCCGAAGGCGAGTCTGGC 102

RESULT 27

B1832654/c

LOCUS

603082033F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5221137 5',

DEFINITION

mRNA sequence.

ACCESSION

B1832654

VERSION

B1832654.1 GI:15944204

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE

1 (bases 1 to 682)

AUTHORS

NIH-MGC http://mgc.nci.nih.gov/.

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.

EMAIL

cgagbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

http://image.lnl.gov

Plate: LRAM1556 row: a column: 10

High quality sequence stop: 680.

Location/Qualifiers

1. 682

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5221137"

/lab_host="DH10B"

/clone_id="NIH_MGC_120"

/note="Organ: pooled pancreas and spleen; Vector:

PCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA

source anonymous pool of spleen and pancreas from 28 yo

male. Library is oligo-dt primed and directionally cloned

(EcoRV site is destroyed upon cloning). Average insert

size 1.5 Kb, insert size range 1-2.5 Kb. Library is

normalized and enriched for full-length clones and was

constructed by C. Gruber (Invitrogen). Research Genetics

tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 682;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CCCGAAGGCGAGTCTGGC 18
105 CCCGAAGGCGAGTCTGGC 88

```

RESULT 28
AU121050/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
COMMENT
TITLE
JOURNAL
COMMENT
FEATURES
source
1..688
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="HEMB1001969"
/tissue_type="whole embryo, mainly body"
/dev_stage="embryo, 10 weeks"
/clone_lib="HEMB1"
/note="Vector: pME18SF13"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 18; DB 9; Length 688;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1
131
CCCGAAGGCGAGTCTGCG 114

RESULT 29
AU124510/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
COMMENT
TITLE
JOURNAL
COMMENT
FEATURES
source
1..694
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5457909"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 47"
/note="Organ. Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit"

```

```

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.

FEATURES
source
1..694
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RM4000122"
/cell_type="teratocarcinoma"
/cell_line="NT2"
/clone_lib="NT2RM4"
/note="Vector: pME18SF13; mRNA from uninduced NT2 neuronal precursor cells"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 18; DB 9; Length 694;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
1
133
CCCGAAGGCGAGTCTGCG 116

RESULT 30
BM011389/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source
1..707
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5457909"
/tissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 47"
/note="Organ. Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit"

```

ORIGIN (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC library."

Query Match 100.0%; Score 18; DB 12; Length 707;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGTCTGGC 18
DB 118 CCCGAGAGCAGTCTGGC 101

RESULT 31
LOCUS AU141723/c 723 bp mRNA linear EST 05-AUG-2002
DEFINITION AU141723 THYR01 Homo sapiens cDNA clone THYR0100106 5', mRNA
sequence.
ACCESSION AU141723 GI:11003244
VERSION AU141723
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 723)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel.: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers

FEATURES
source 1..723
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="THYR0100106"
/tissue_type="thyroid gland"
/clone_lib="THYR01"
/note="Vector: pME18SFL3"

ORIGIN
Query Match 100.0%; Score 18; DB 9; Length 723;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGTCTGGC 18
DB 137 CCCGAGAGCAGTCTGGC 120

RESULT 32
LOCUS AU131952/c 724 bp mRNA linear EST 01-AUG-2002
DEFINITION AU131952 NT2RP3 Homo sapiens cDNA clone NT2RP3003525 5', mRNA
sequence.
ACCESSION AU131952 GI:10992306
VERSION AU131952
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

ORIGIN
Query Match 100.0%; Score 18; DB 9; Length 723;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

REFERENCE 1 (bases 1 to 724)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel.: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers

FEATURES
source 1..724
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP3003525"
/cell_type="keratinocarcinoma"
/cell_line="HT2"
/clone_lib="NT2RP3"
/note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
cells after 2-weeks retinoic acid (RA) induction"

ORIGIN
Query Match 100.0%; Score 18; DB 9; Length 724;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGTCTGGC 18
DB 132 CCCGAGAGCAGTCTGGC 115

RESULT 33
LOCUS BM012402/c 726 bp mRNA linear EST 30-OCT-2001
DEFINITION BM012402 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5459560 5',
mRNA sequence.
ACCESSION BM012402
VERSION BM012402
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 726)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L10M1962 row: o column: 17
High quality sequence stop: 542.
Location/Qualifiers

FEATURES
source 1..726
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5459560"

/cissue_type="neuroblastoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH_MGC_47"
/note="Organ: brain; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 726;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGGCACTGTGGC 18
123 CCCGAGAGGCACTGTGGC 106

Db

RESULT 34
AUI41300/c AUI41300 729 bp mRNA linear EST 05-ANG-2002
LOCUS AUI41300 THYR01 Homo sapiens cDNA clone THYR01000362 5', mRNA
DEFINITION sequence.
ACCESSION AUI41300
VERSION AUI41300.1 GI:11002821
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 729)
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,
Yamamoto, U., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and
Iwagaki, T.

AUTHORS

TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Iwagaki
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kiserazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.

FEATURES

Location/Qualifiers
1..729
source

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="THYR01000362"
/cissue_type="thyroid gland"
/clone_1ib="THYR01"
/note="Vector: pME18SFL3"

ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 729;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGGCACTGTGGC 18
132 CCCGAGAGGCACTGTGGC 115

Db

RESULT 35

BM048582/c 732 bp mRNA linear EST 07-NOV-2001
LOCUS BM048582
DEFINITION 601623927F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5449735 5',
mRNA sequence.
ACCESSION BM048582
VERSION BM048582.1 GI:16777849
KEYWORDS EST.

SOURCE

Homo sapiens (human)
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 732)
NIH-MGC <http://mgs.nci.nih.gov/>.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov

Tissue Procurement: DCTD/DTF

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LICM1937 row: f column: 08

High quality sequence stop: 715.

FEATURES

Location/Qualifiers

1..732

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5449735"

/cissue_type="carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_1ib="NIH_MGC_40"

/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dt priming;
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 732;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGGCACTGTGGC 18
120 CCCGAGAGGCACTGTGGC 103

Db

RESULT 36

BE273022/c 744 bp mRNA linear EST 13-JUL-2000
LOCUS BE273022
DEFINITION 601171343F1 NIH_MGC_14 Homo sapiens cDNA clone IMAGE:544714 5',
mRNA sequence.

ACCESSION

BE273022

VERSION

BE273022.1 GI:9147377

KEYWORDS

EST.

SOURCE

Homo sapiens (human)
Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE

1 (bases 1 to 744)
NIH-MGC <http://mgs.nci.nih.gov/>.

AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov

Tissue Procurement: DCTD/DTF

CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: image.lnl.gov
Plate: L10CM240 row: f column: 11
High quality sequence stop: 639.

FEATURES

SOURCE

1. 744
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:3544714"

/tissue_type="renal cell adenocarcinoma"

/lab_host="DH10B (phage-resistant)"

/clone_1lb="NIH_MGC_14"

/note="Organ: Kidney; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 18; DB 10; Length 744;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGAAGGAGCTGTGCG 18
|||||
Db 93 CCCGGAAGGAGCTGTGCG 76

RESULT 37
BM048815/c 750 bp mRNA linear EST 07-NOV-2001
LOCUS 603628360F1 NIH_MGC_40 Homo sapiens CDNA clone IMAGE:5456703 5',
DEFINITION
BM048815
RNA sequence.
ACCESSION
BM048815
VERSION
KEYWORDS
EST. GI:16778082

SOURCE
ORGANISM
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 750)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

REFERENCE
AUTHORS
JOURNAL
COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov

Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov

Plate: L10CM955 row: h column: 16
High quality sequence stop: 715.

FEATURES

SOURCE

1. 750
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5456703"

/tissue_type="carcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

/clone_1lb="NIH_MGC_40"

/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; CDNA made by oligo-dT priming."

Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGGAG(G). Library constructed by Ling Hong in the Laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 750;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGAAGGAGCTGTGCG 18
|||||
Db 120 CCCGGAAGGAGCTGTGCG 103

RESULT 38
B1839050/c 758 bp mRNA linear EST 04-OCT-2001
LOCUS 603083048F1 NIH_MGC_120 Homo sapiens CDNA clone IMAGE:5222266 5',
DEFINITION
B1839050
RNA sequence.
ACCESSION
B1839050
VERSION
KEYWORDS
EST. GI:15950600

SOURCE
ORGANISM
Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 758)

NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

REFERENCE
AUTHORS
JOURNAL
COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov

Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at:
http://image.lnl.gov

Plate: L1AM1558 row: p column: 11
High quality sequence start: 42

High quality sequence stop: 519.

FEATURES

SOURCE

1. 758
/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:5222266"

/lab_host="DH10B"

/clone_1lb="NIH_MGC_120"

/note="Organ: pooled pancreas and spleen; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: EcoRI (destroyed), RNA source anonymous pool of spleen and pancreas from 28 yo male. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.5 kb, insert size range 1-2.5 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 025. Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 758;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGAAGGAGCTGTGCG 18
|||||
Db 146 CCCGGAAGGAGCTGTGCG 129

```

RESULT 39
BX462478/c 762 bp mRNA linear EST 22-MAY-2003
LOCUS BX462478 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens cDNA
DEFINITION clone CSODH003Y003 5-PRIME, mRNA sequence.
ACCESSION BX462478
VERSION BX462478.1 GI:31033411
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Li, W.B., Gruber, C., Jesssee, J. and Polayres, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8550.f. For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODH003AH02QPLcluster=8550.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODH003AH02QPL.

FEATURES
Source
1..762
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODH003Y003"
/tissue_type="T CELLS (JURKAT CELL LINE)"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE)"
/Note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
with a NotI-oligo (dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN
Query Match 100.0%; Score 18; DB 13; Length 762;
Best Local Similarity 100.0%; Pred. No. 5,9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTGTGGC 18
Db 178 CCCGAGAGCAGCTGTGGC 161

RESULT 40
BM044564/c 765 bp mRNA linear EST 07-NOV-2001
LOCUS BM044564 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5447739 5',
DEFINITION mRNA sequence.
ACCESSION BM044564
VERSION BM044564.1 GI:16773831
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNCM1932 row: c column: 04
High quality sequence stop: 755.
Location/Qualifiers
1..765
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5447739"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/Note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACGCGG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 100.0%; Score 18; DB 12; Length 765;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTGTGGC 18
Db 120 CCCGAGAGCAGCTGTGGC 103

RESULT 41
BM046401/c 765 bp mRNA linear EST 07-NOV-2001
LOCUS BM046401 6036242EF1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5452758 5',
DEFINITION mRNA sequence.
ACCESSION BM046401
VERSION BM046401.1 GI:16775668
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.lnl.gov
Plate: LNCM1945 row: d column: 07
High quality sequence stop: 544.
Location/Qualifiers
1..765
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5452758"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/Note="Organ: prostate; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cDNA made by oligo-dT priming.
Library was constructed by Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory"

```


Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley), using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 765;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGGACAGTCTGGC 18
DB 120 CCCGAGAGGACAGTCTGGC 103

RESULT 42

BM048326 765 bp mRNA linear EST 07-NOV-2001
LOCUS BM048326/c
DEFINITION 603625546F1 NIH_MGC_40 Homo sapiens cDNA clone IMAGE:5452187 5',
mRNA sequence.

ACCESSION BM048326
VERSION BM048326.1 GI:16777593
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (bases 1 to 765)
NIH-MGC <http://mgs.nci.nih.gov/>.

AUTHORS

JOURNAL

COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM1943 row: 1 column: 12
High quality sequence stop: 341.
Location/Qualifiers

FEATURES

source

1..765
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5452187"
/tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_40"
/note="Organ: prostate; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 765;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGGACAGTCTGGC 18
DB 115 CCCGAGAGGACAGTCTGGC 98

RESULT 43

BG481823/c

LOCUS BG481823 767 bp mRNA linear EST 21-MAR-2001
DEFINITION 602529221F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4652690 5',
mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: LLCM1437 row: 1 column: 03
High quality sequence stop: 755.
Location/Qualifiers

FEATURES

source

1..767
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4652690"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCAAGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 767;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGGACAGTCTGGC 18
DB 110 CCCGAGAGGACAGTCTGGC 93

RESULT 44

LOCUS

AU120569 781 bp mRNA linear EST 01-AUG-2002
DEFINITION AU120569 HENB1 Homo sapiens cDNA clone HENB100956 5', mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

JOURNAL

COMMENT

Unpublished (2000)
Contact: Takao Isogai

Genomics Laboratory
 Helix Research Institute
 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
 Tel: 81-438-52-3975
 Fax: 81-438-52-3986
 Email: genomics@hri.co.jp
 HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
 Research Institute; cDNA library construction; Department of
 Virology, Institute of Medical Science, University of Tokyo, and
 Helix Research Institute.

FEATURES

source
 1..781
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HEMBA1000956"
 /tissue_type="whole embryo, mainly body"
 /dev_stage="embryo, 10 weeks"
 /clone_id="HEMBA1"
 /note="Vector: pME18SFL3"

ORIGIN

Query Match 100.0%; Score 18; DB 9; Length 781;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCCGGAAGGCGAGTCTGGC 18
 133 CCCGGAAGGCGAGTCTGGC 116

RESULT 45 808 bp mRNA linear EST 04-OCT-2001
 LOCUS B1821174/c
 DEFINITION 603035073p1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5175858 5',
 mRNA sequence.

ACCESSION B1821174
 VERSION B1821174.1 GI:15932724
 KEYWORDS EST.

SOURCE
 ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 808)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 http://image.lnl.gov

Plate: L1AM1438 row: b column: 19
 High quality sequence stop: 802.
 Location/Qualifiers

FEATURES

source
 1..808
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5175858"
 /lab_host="DH108"

/clone_id="NIH_MGC_115"
 /note="Organ: pooled brain, lung, testis; Vector:
 pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 6 male brains, age range 23-27; 1
 male lung, age 27; and 1 male testis, age 69. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.8 kb,
 insert size range 1-3 kb. Library is normalized and

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 808;
 Best Local Similarity 100.0%; Pred. No. 6e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCCGGAAGGCGAGTCTGGC 18
 104 CCCGGAAGGCGAGTCTGGC 87

RESULT 46 815 bp mRNA linear EST 16-OCT-2001
 LOCUS B1905893/c
 DEFINITION 603063028p1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212086 5',
 mRNA sequence.

ACCESSION B1905893
 VERSION B1905893.1 GI:16168494
 KEYWORDS EST.

SOURCE
 ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 815)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LINL at:
 http://image.lnl.gov

Plate: L1AM1532 row: h column: 07
 High quality sequence stop: 778.
 Location/Qualifiers

FEATURES

source
 1..815
 Location/Qualifiers

/organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5212086"
 /tissue_type="leukocyte"
 /lab_host="DH108"

/clone_id="NIH_MGC_118"
 /note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV
 (destroyed); RNA source leukocytes from anonymous pool of
 non-activated adult donors. Library is oligo-dT primed
 and directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.7 kb, insert size range
 1.2-3.3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 027. Note:
 this is a NIH_MGC Library."

ORIGIN

Query Match 100.0%; Score 18; DB 12; Length 815;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CCCGGAAGGCGAGTCTGGC 18
 116 CCCGGAAGGCGAGTCTGGC 99

RESULT 47 817 bp mRNA linear EST 17-OCT-2002
 LOCUS B1902747/c
 B1902747

enriched for full-length clones and was constructed by C.
 Gruber (Invitrogen). Research Genetics tracking code
 021. Note: this is a NIH_MGC Library."

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: March 5, 2004, 00:34:26 ; Search time 270 Seconds
(without alignments)

243.829 Million cell updates/sec

Title: US-09-848-868-35

Perfect score: 18

Sequence: 1 cccgaagagcagctcggc 18

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 2421054 seqs, 1828716029 residues

Total number of hits satisfying chosen parameters: 4842108

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database : Published Applications_NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US05_PUBCOMB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US04_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US03_PUBCOMB.seq.*
6: /cgn2_6/ptodata/2/pubpna/US02_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US01_PUBCOMB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
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16: /cgn2_6/ptodata/2/pubpna/US02_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US01_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	18	100.0	133	9	US-09-848-868-36
4	18	100.0	1303	15	US-10-397-635-6
5	18	100.0	1307	9	US-09-732-384-8
6	18	100.0	1317	10	US-09-829-922-1
7	18	100.0	1317	14	US-10-160-290-1
8	18	100.0	1760	10	US-09-849-602-9
9	18	100.0	1760	15	US-10-191-121-4
10	18	100.0	2209	15	US-10-063-674-2065
11	18	100.0	2521	15	US-10-428-802-25
12	18	100.0	2521	15	US-10-430-503-16
13	18	100.0	2629	12	US-10-391-068-1
14	18	100.0	2629	14	US-10-077-176-58
15	18	100.0	2629	14	US-10-077-176-58

16	18	100.0	2629	14	US-10-077-176-60	Sequence 60, Appl
17	18	100.0	2629	14	US-10-077-176-61	Sequence 61, Appl
18	100.0	2629	15	US-10-439-388-16	Sequence 16, Appl	
19	18	100.0	2629	15	US-10-165-216-3	Sequence 3, Appl
20	18	100.0	2629	15	US-10-159-563-188	Sequence 188, App
21	16.4	91.1	436	10	US-09-918-995-36880	Sequence 36880, A
22	16.4	91.1	905	14	US-10-066-453-113	Sequence 113, App
23	16.4	91.1	942	9	US-09-764-847-1845	Sequence 1845, Ap
24	16.4	91.1	942	9	US-09-764-847-1846	Sequence 1846, Ap
25	16.4	91.1	942	14	US-10-092-154-1845	Sequence 1845, Ap
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Sequence 623, App
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C 180 13.8 76.7 150 12 US-10-085-783A-4976
C 181 13.8 76.7 150 15 US-10-242-535A-4976
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C 199 13.8 76.7 396 9 US-09-796-692-3571
C 200 13.8 76.7 396 14 US-10-040-862-3571

ALIGNMENTS

US-09-848-868-35
Sequence 35, Application US/09848868
Publication No. US2003016586A1
GENERAL INFORMATION:
APPLICANT: Iversen, Patrick L.
INVENTOR: Hudziak, Robert
TITLE OF INVENTION: Splice-Region Antisense Composition and
METHOD OF INVENTION: Splice-Region Antisense Composition and
FILE REFERENCE: 0450-0037.30
CURRENT APPLICATION NUMBER: US/09/848, 868
CURRENT FILING DATE: 2003-05-04
PRIOR APPLICATION NUMBER: US 60/202,376
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 35
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense
US-09-848-868-35
Query Match 100.0% Score 18; DB 10; Length 18;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CCCGAAGGCGAGTCTGGC 18

Db 1 CCCGAGGAGCTGAC 18

RESULT 2

US-09-848-868-36
Sequence 36, Application US/09848868
Publication No. US20030166588A1
GENERAL INFORMATION:
APPLICANT: Iversen, Patrick L.
APPLICANT: Hudziak, Robert
TITLE OF INVENTION: Splice-region Antisense Composition and
TITLE OF INVENTION: Method
FILE REFERENCE: 0450-0037.30
CURRENT APPLICATION NUMBER: US/09/848,868
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: US 60/202,376
PRIOR FILING DATE: 2000-05-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 36
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: antisense
US-09-848-868-36

Query Match 100.0%; Score 18; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCTGAC 18
Db 17 CCCGAGGAGCTGAC 34

RESULT 3

US-09-776-695-22/c
Sequence 22, Application US/09776695
Patent No. US20020068283A1
GENERAL INFORMATION:
APPLICANT: Boeke, Jef

Brachmann, Rainer
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING P53
MUTATIONS WHICH SUPPRESS P53 CANCER MUTA- TIONS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/776,695
FILING DATE: 26-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,006
FILING DATE: 2001-03-28

ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.03170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299

TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-776-695-22

Query Match 100.0%; Score 18; DB 9; Length 133;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCTGAC 18
Db 35 CCCGAGGAGCTGAC 18

RESULT 4

US-10-397-635-6/c
Sequence 6, Application US/10397635
Publication No. US2004009604A1
GENERAL INFORMATION:
APPLICANT: ZHANG, XIAOLI
APPLICANT: FU, XUPING
TITLE OF INVENTION: POTENT ONCOLYTIC HERPES SIMPLEX VIRUS FOR CANCER
TITLE OF INVENTION: THERAPY
FILE REFERENCE: P02410US2
CURRENT APPLICATION NUMBER: US/10/397,635
CURRENT FILING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: 60/367,788
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 60/410,024
PRIOR FILING DATE: 2002-09-11
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 1303
TYPE: DNA
ORGANISM: Homo sapiens
US-10-397-635-6

Query Match 100.0%; Score 18; DB 15; Length 1303;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCTGAC 18
Db 113 CCCGAGGAGCTGAC 96

RESULT 5

US-09-732-384-8/c
Sequence 8, Application US/09732384
Patent No. US20020132977A1
GENERAL INFORMATION:
APPLICANT: Yuan, Zhi-Min
APPLICANT: Gu, Jijie
TITLE OF INVENTION: Inhibition of p53 Degradation
FILE REFERENCE: 21508-044
CURRENT APPLICATION NUMBER: US/09/732,384
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: 60/169,816
PRIOR FILING DATE: 1999-12-08
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 1307
TYPE: DNA
ORGANISM: Homo sapiens
US-09-732-384-8

Query Match 100.0%; Score 18; DB 9; Length 1307;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGGC 18
DB 117 CCCGGAAGCAGCTGGC 100

RESULT 6

US-09-829-922-1/c
; Sequence 1, Application US/09829922
; Publication No. US20030171537A1
; GENERAL INFORMATION:
; APPLICANT: Halazoneis, Thanos
; TITLE OF INVENTION: Peptides and peptidomimetics with
; TITLE OF INVENTION: structural similarity to human p53 that activate p53
; FILE REFERENCE: 2973.19998
; CURRENT APPLICATION NUMBER: US/09/829,922
; PRIOR FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 08/894,327
; PRIOR FILING DATE: 1997-12-04
; PRIOR APPLICATION NUMBER: pctus96/01535
; PRIOR FILING DATE: 1996-02-16
; PRIOR APPLICATION NUMBER: 08/392,542
; PRIOR FILING DATE: 1995-02-16
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1317
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-829-922-1

Query Match 100.0%; Score 18; DB 10; Length 1317;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGGC 18
DB 127 CCCGGAAGCAGCTGGC 110

RESULT 7

US-10-160-290-1/c
; Sequence 1, Application US/10160290
; Publication No. US20030124557A1
; GENERAL INFORMATION:
; APPLICANT: Halazoneis, Thanos
; TITLE OF INVENTION: Peptides and peptidomimetics with
; TITLE OF INVENTION: Structural Similarity to Human p53 That Activate
; p53
; FUNCTION
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie & Beckett
; STREET: 1001 G Street, N.W.
; CITY: Washington, D.C.
; STATE: District of Columbia
; COUNTRY: U.S.
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/160,290
; FILING DATE: 04-Jun-2002
; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/685,027
FILING DATE: 10-Oct-2000
APPLICATION NUMBER: 08/392,542
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 0486,4839
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-160-290-1

Query Match 100.0%; Score 18; DB 14; Length 1317;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGGC 18
DB 127 CCCGGAAGCAGCTGGC 110

RESULT 8

US-09-849-602-9/c
; Sequence 9, Application US/09849602
; Publication No. US20030165834A1
; GENERAL INFORMATION:
; APPLICANT: Scanlan, Matthew J.
; APPLICANT: Old, Lloyd J.
; APPLICANT: Stockert, Elisabeth
; APPLICANT: Chen, Yao-Tseng
; TITLE OF INVENTION: Colon Cancer Antigen Panel
; FILE REFERENCE: U0461/1105(JRV)
; CURRENT APPLICATION NUMBER: US/09/849,602
; CURRENT FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-849-602-9

Query Match 100.0%; Score 18; DB 10; Length 1760;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGGC 18
DB 206 CCCGGAAGCAGCTGGC 189

RESULT 9

US-10-191-121-4/c
; Sequence 4, Application US/10191121
; Publication No. US20040005574A1
; GENERAL INFORMATION:
; APPLICANT: Guarente, Leonard
; APPLICANT: Vaziri, Homayoun
; APPLICANT: Imai, Shin-Ichiro
; APPLICANT: Gu, Wei
; TITLE OF INVENTION: Sir2 and p53 Deacetylation

```
FILE REFERENCE: 13407-015002
CURRENT APPLICATION NUMBER: US/10/191,121
CURRENT FILING DATE: 2002-07-08
PRIOR APPLICATION NUMBER: US 60/303,456
PRIOR FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: US 10/NNN,NNN
PRIOR FILING DATE: 2002-07-05
PRIOR APPLICATION NUMBER: US 60/303,370
PRIOR FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 1760
TYPE: DNA
ORGANISM: Homo sapiens
US-10-191-121-4

Query Match
Best Local Similarity 100.0%; Score 18; DB 15; Length 1760;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCGGAAGGCGAGCTGGC 18
Db 206 CCCGGAAGGCGAGCTGGC 189

RESULT 10
US-10-062-674-2065/c
Sequence 2065, Application US/10062674
Publication No. US20040005559A1
GENERAL INFORMATION:
APPLICANT: LOIING, JEANNE F.; KASER, MATTHEW R.
TITLE OF INVENTION: MARKERS OF NEURONAL DIFFERENTIATION AND MORPHOGENESIS
FILE REFERENCE: PA-0026-1 CIP
CURRENT APPLICATION NUMBER: US/10/062,674
CURRENT FILING DATE: 2002-01-30
PRIOR APPLICATION NUMBER: US 09/625,102
PRIOR FILING DATE: 2000-07-24
NUMBER OF SEQ ID NOS: 2217
SOFTWARE: PERL Program
SEQ ID NO 2065
LENGTH: 2209
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. US20040005559A1 430224.2
US-10-062-674-2065

Query Match
Best Local Similarity 100.0%; Score 18; DB 15; Length 2209;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCGGAAGGCGAGCTGGC 18
Db 170 CCCGGAAGGCGAGCTGGC 153

RESULT 11
US-10-429-802-25/c
Sequence 25, Application US/10429802
Publication No. US20030228285A1
GENERAL INFORMATION:
APPLICANT: HUNG, MIEN-CHIE
APPLICANT: ZOU, YIYU
TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF)-RESPONSIVE PROMOTER
FILE REFERENCE: UTSC:752US
CURRENT APPLICATION NUMBER: US/10/429,802
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: 60/377,672
PRIOR FILING DATE: 2002-05-03
NUMBER OF SEQ ID NOS: 54
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 2521
TYPE: DNA
ORGANISM: Homo sapiens
US-10-429-802-25

Query Match
Best Local Similarity 100.0%; Score 18; DB 15; Length 2521;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCGGAAGGCGAGCTGGC 18
Db 127 CCCGGAAGGCGAGCTGGC 110

RESULT 12
US-10-430-503-16/c
Sequence 16, Application US/10430503
Publication No. US20040005684A1
GENERAL INFORMATION:
APPLICANT: HUNG, MIEN-CHIE
APPLICANT: LAN, KENG-LI
APPLICANT: OU-YANG, FU
APPLICANT: LIU, JAW-CHING
APPLICANT: LAN, KENG-HSIN
TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC
FILE REFERENCE: UTSC:797US
CURRENT APPLICATION NUMBER: US/10/430,503
CURRENT FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 60/383,063
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 16
LENGTH: 2521
TYPE: DNA
ORGANISM: Homo sapiens
US-10-430-503-16

Query Match
Best Local Similarity 100.0%; Score 18; DB 15; Length 2521;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCGGAAGGCGAGCTGGC 18
Db 127 CCCGGAAGGCGAGCTGGC 110

RESULT 13
US-10-391-068-1/c
Sequence 1, Application US/10391068
Publication No. US20040028654A1
GENERAL INFORMATION:
APPLICANT: UT, LIN
APPLICANT: ROTH, JACK
TITLE OF INVENTION: PROTAINE-ADENOVIRAL VECTOR COMPLEXES
FILE REFERENCE: INRP:097US
CURRENT APPLICATION NUMBER: US/10/391,068
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: 60/366,846
PRIOR FILING DATE: 2002-03-22
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
LENGTH: 2625
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (252)...(1433)
```

US-10-391-068-1

Query Match 100.0%; Score 18; DB 12; Length 2625;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
|||||
DB 243 CCGGAGGCGAGTCTGGC 226

RESULT 14
US-10-077-176-58/c
; Sequence 58, Application US/10077176
; Publication No. US20030175862A1
; GENERAL INFORMATION:
; APPLICANT: Brachmann, Rainer
; TITLE OF INVENTION: ENGINEERED OPEN READING FRAME FOR P53
; FILE REFERENCE: 004255.00008
; CURRENT APPLICATION NUMBER: US/10/077,176
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 58
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-077-176-58

Query Match 100.0%; Score 18; DB 14; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
|||||
DB 243 CCGGAGGCGAGTCTGGC 226

RESULT 15
US-10-077-176-59/c
; Sequence 59, Application US/10077176
; Publication No. US20030175862A1
; GENERAL INFORMATION:
; APPLICANT: Brachmann, Rainer
; TITLE OF INVENTION: ENGINEERED OPEN READING FRAME FOR P53
; FILE REFERENCE: 004255.00008
; CURRENT APPLICATION NUMBER: US/10/077,176
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-077-176-59

Query Match 100.0%; Score 18; DB 14; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
|||||
DB 243 CCGGAGGCGAGTCTGGC 226

RESULT 16
US-10-077-176-60/c
; Sequence 60, Application US/10077176
; Publication No. US20030175862A1
; GENERAL INFORMATION:
; APPLICANT: Brachmann, Rainer
; TITLE OF INVENTION: ENGINEERED OPEN READING FRAME FOR P53
; FILE REFERENCE: 004255.00008

CURRENT APPLICATION NUMBER: US/10/077,176
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-077-176-60

Query Match 100.0%; Score 18; DB 14; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
|||||
DB 243 CCGGAGGCGAGTCTGGC 226

RESULT 17
US-10-077-176-61/c
; Sequence 61, Application US/10077176
; Publication No. US20030175862A1
; GENERAL INFORMATION:
; APPLICANT: Brachmann, Rainer
; TITLE OF INVENTION: ENGINEERED OPEN READING FRAME FOR P53
; FILE REFERENCE: 004255.00008
; CURRENT APPLICATION NUMBER: US/10/077,176
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-077-176-61

Query Match 100.0%; Score 18; DB 14; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
|||||
DB 243 CCGGAGGCGAGTCTGGC 226

RESULT 18
US-10-439-388-16/c
; Sequence 16, Application US/10439388
; Publication No. US20030228617A1
; GENERAL INFORMATION:
; APPLICANT: Aune, Thomas M
; APPLICANT: Olsen, Nancy J
; TITLE OF INVENTION: Method for Predicting Autoimmune Disease
; FILE REFERENCE: 1242/68
; CURRENT APPLICATION NUMBER: US/10/439,388
; CURRENT FILING DATE: 2003-05-16
; PRIOR APPLICATION NUMBER: US 60/381,055
; PRIOR FILING DATE: 2002-05-16
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-439-388-16

Query Match 100.0%; Score 18; DB 15; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGTCTGGC 18
|||||

Db 243 CCCGAGGAGCTCTGGC 226

RESULT 19
US-10-165-216-3/c
; Sequence 3, Application US/10165216
; Publication No. US20030228675A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Diane M.
; APPLICANT: Abraham, Robert T.
; TITLE OF INVENTION: ATM Related Kinase ATX, Nucleic Acids
; FILE REFERENCE: P-LJ 5222
; CURRENT APPLICATION NUMBER: US/10/165,216
; CURRENT FILING DATE: 2002-06-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (252)...(1433)
US-10-165-216-3

Query Match 100.0%; Score 18; DB 15; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCTCTGGC 18
|||||

Db 243 CCCGAGGAGCTCTGGC 226

RESULT 20
US-10-159-563-188/c
; Sequence 188, Application US/10159563
; Publication No. US20040009154A1
; GENERAL INFORMATION:
; APPLICANT: Khan, Javed
; APPLICANT: Ringner, Markus
; APPLICANT: Peterson, Carsten
; APPLICANT: Meltzer, Paul
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR
; TITLE OF INVENTION: DIAGNOSIS AND FOR TREATING THE THERAPY OF SELECT CANCERS
; FILE REFERENCE: 11613, 56US11
; CURRENT APPLICATION NUMBER: US/10/159,563
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: US 10/133,937
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 444
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 188
; LENGTH: 2629
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-159-563-188

Query Match 100.0%; Score 18; DB 15; Length 2629;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCTCTGGC 18
|||||

Db 243 CCCGAGGAGCTCTGGC 226

RESULT 21
US-09-918-995-36880/c
; Sequence 36880, Application US/09918995
; Publication No. US2003007363A1
; GENERAL INFORMATION:

; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36880
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-918-995-36880

Query Match 91.1%; Score 16.4; DB 10; Length 436;
Best Local Similarity 94.4%; Pred. No. 56;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCTCTGGC 18
|||||

Db 90 CCCGAGGAGCTCTGGC 73

RESULT 22
US-10-066-543-113/c
; Sequence 113, Application US/10066543
; Publication No. US2003008781B1
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yugu
; APPLICANT: Pyle, Ruth A.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Carter, Derrick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Smith, Carole L.
; APPLICANT: Durham, Margareta
; APPLICANT: Stoik, John A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.563
; CURRENT APPLICATION NUMBER: US/10/066,543
; CURRENT FILING DATE: 2002-01-31
; NUMBER OF SEQ ID NOS: 3417
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 113
; LENGTH: 905
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 13, 45, 386, 545, 580, 582, 584, 590, 591, 603, 606, 609,
; LOCATION: 610, 616, 621, 623, 624, 625, 629, 630, 646, 652, 670, 672,
; LOCATION: 674, 676, 688, 700, 709, 710, 744, 753, 756, 758, 759, 763,
; LOCATION: 786, 796, 823, 851, 876, 885
; OTHER INFORMATION: n = A,T,C or G
US-10-066-543-113

Query Match 91.1%; Score 16.4; DB 14; Length 905;
Best Local Similarity 94.4%; Pred. No. 51;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGAGGAGCTCTGGC 18
|||||

Db 516 CCCGAGGAGCTCTGGC 499

RESULT 23
US-09-764-847-1845/c
; Sequence 1845, Application US/09764847

```
/ Patent No. US20020132767A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PC009
/ CURRENT APPLICATION NUMBER: US/09/764,847
/ CURRENT FILING DATE: 2001-01-17
/ Prior application data removed - consult PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 2003
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1845
/ LENGTH: 942
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-764-847-1845

Query Match
Best Local Similarity 91.1%; Score 16.4; DB 9; Length 942;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCGAGTCTGGC 18
Db 58 CCCGGAAGGCGAGTCTGTC 41

RESULT 24
/ US-09-764-847-1846/c
/ Sequence 1846, Application US/09764847
/ Patent No. US20020132767A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PC009
/ CURRENT APPLICATION NUMBER: US/09/764,847
/ CURRENT FILING DATE: 2001-01-17
/ Prior application data removed - consult PALM or file wrapper
/ NUMBER OF SEQ ID NOS: 2003
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1846
/ LENGTH: 942
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-764-847-1846

Query Match
Best Local Similarity 91.1%; Score 16.4; DB 9; Length 942;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCGAGTCTGGC 18
Db 58 CCCGGAAGGCGAGTCTGTC 41

RESULT 25
/ US-10-092-154-1845/c
/ Sequence 1845, Application US/10092154
/ Publication No. US20030054375A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PC009c1
/ CURRENT APPLICATION NUMBER: US/10/092,154
/ CURRENT FILING DATE: 2002-03-07
/ NUMBER OF SEQ ID NOS: 2003
/ Prior application removed - See file wrapper or Palm
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1845
/ LENGTH: 942
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-092-154-1845

Query Match
91.1%; Score 16.4; DB 14; Length 942;
Score 16.4; DB 14; Length 942;

QY 1 CCCGGAAGGCGAGTCTGGC 18
Db 58 CCCGGAAGGCGAGTCTGTC 41

RESULT 26
/ US-10-092-154-1846/c
/ Sequence 1846, Application US/10092154
/ Publication No. US20030054375A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: PC009c1
/ CURRENT APPLICATION NUMBER: US/10/092,154
/ CURRENT FILING DATE: 2002-03-07
/ NUMBER OF SEQ ID NOS: 2003
/ Prior application removed - See file wrapper or Palm
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1846
/ LENGTH: 942
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-092-154-1846

Query Match
Best Local Similarity 91.1%; Score 16.4; DB 14; Length 942;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCGAGTCTGGC 18
Db 58 CCCGGAAGGCGAGTCTGTC 41

RESULT 27
/ US-09-765-231A-2/c
/ Sequence 2, Application US/09765231A
/ Patent No. US2002019452A1
/ GENERAL INFORMATION:
/ APPLICANT: Searle/Konsanto
/ APPLICANT: Philipard, Deborah
/ APPLICANT: Vasanthakumari, Geetha
/ APPLICANT: Dotson, Stanton
/ APPLICANT: Ma, Xiao-Jun
/ TITLE OF INVENTION: Osteoarthritis tissue-derived nucleic acids, polypeptides,
/ TITLE OF INVENTION: vectors, and cells
/ FILE REFERENCE: SO-3221 PR
/ CURRENT APPLICATION NUMBER: US/09/765,231A
/ CURRENT FILING DATE: 2001-01-18
/ NUMBER OF SEQ ID NOS: 82
/ SEQ ID NO 2
/ LENGTH: 1986
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-09-765-231A-2

Query Match
Best Local Similarity 91.1%; Score 16.4; DB 9; Length 1986;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCGAGTCTGGC 18
Db 893 CCCGGAAGGCGAGTCTGGC 876

RESULT 28
/ US-09-884-441-332
/ Sequence 332, Application US/09884441
/ Patent No. US20020119158A1
/ GENERAL INFORMATION:
/ APPLICANT: Algate, Paul A.
```

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; APPLICANT: Carter, Darick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C7
; CURRENT APPLICATION NUMBER: US/09/884,441
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 184
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-884-441-332

Query Match      85.6%; Score 15.4; DB 9; Length 184;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CCGAAGGCGAGTCTGGC 18
DB      112 CCAGAAGGCGAGTCTGGC 128

RESULT 29
US-09-907-969-332
; Sequence 332, Application US/09907969
; Publication No. US20030091580A1
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Aldate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Hill, Paul
; APPLICANT: Albone, Earl
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C8
; CURRENT APPLICATION NUMBER: US/09/907,969
; CURRENT FILING DATE: 2001-07-17
; NUMBER OF SEQ ID NOS: 596
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 332
; LENGTH: 184
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-907-969-332

Query Match      85.6%; Score 15.4; DB 10; Length 184;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CCGAAGGCGAGTCTGGC 18
DB      112 CCAGAAGGCGAGTCTGGC 128

RESULT 30
US-09-827-271-332
; Sequence 332, Application US/09827271
; Publication No. US20030165504A1
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
```

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; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 332
; LENGTH: 184
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-827-271-332

Query Match      85.6%; Score 15.4; DB 10; Length 184;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CCGAAGGCGAGTCTGGC 18
DB      112 CCAGAAGGCGAGTCTGGC 128

RESULT 31
US-10-198-053-332
; Sequence 332, Application US/10198053
; Publication No. US20030124140A1
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 332
; LENGTH: 184
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-053-332

Query Match      85.6%; Score 15.4; DB 14; Length 184;
Best Local Similarity 94.1%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 CCGAAGGCGAGTCTGGC 18
DB      112 CCAGAAGGCGAGTCTGGC 128

RESULT 32
US-10-085-783A-47890/C
; Sequence 47890, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47890
; LENGTH: 358
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-47890
```

Query Match 85.6%; Score 15.4; DB 12; Length 358;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 358 CCGAAGGCACTCTGGC 342

RESULT 33
US-10-242-535A-47890/c
Sequence 47890, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 47890
LENGTH: 358
TYPE: DNA
ORGANISM: Human
US-10-242-535A-47890

Query Match 85.6%; Score 15.4; DB 15; Length 358;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 358 CCGAAGGCACTCTGGC 342

RESULT 34
US-10-085-783A-21425/c
Sequence 21425, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21425
LENGTH: 371
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:

NAME/KEY: misc_feature
LOCATION: (203)..(203)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (205)..(206)
OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-21425

Query Match 85.6%; Score 15.4; DB 12; Length 371;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 165 CCGAAGGCACTCTGGC 149

RESULT 35
US-10-242-535A-21425/c
Sequence 21425, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21425
LENGTH: 371
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(1)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (203)..(203)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (205)..(206)
OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-21425

Query Match 85.6%; Score 15.4; DB 15; Length 371;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 165 CCGAAGGCACTCTGGC 149

RESULT 36
US-10-085-783A-9459/c
Sequence 9459, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.

PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23153
LENGTH: 397
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (36)..(56)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (67)..(68)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (212)..(212)
OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-23153

Query Match 85.6%; Score 15.4; DB 15; Length 397;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGSC 18
DB 85 CCGAAGGCACTCTGSC 69

RESULT 40
US-10-085-783A-23042/C
Sequence 23042, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liaw, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23042
LENGTH: 399
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (42)..(42)
OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-23042

Query Match 85.6%; Score 15.4; DB 12; Length 399;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGSC 18
DB 351 CCGAAGGCACTCTGSC 335

RESULT 41
US-10-242-535A-23042/C
Sequence 23042, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liaw, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23042
LENGTH: 399
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (42)..(42)
OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-23042

Query Match 85.6%; Score 15.4; DB 15; Length 399;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGSC 18
DB 351 CCGAAGGCACTCTGSC 335

RESULT 42
US-10-085-783A-23133/C
Sequence 23133, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liaw, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23133
LENGTH: 400
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(7)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (40)..(40)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature

LOCATION: (48)..(48)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (341)..(341)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (394)..(394)
OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-23133

Query Match 85.6%; Score 15.4; DB 12; Length 400;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 36 CCGAAGGCACTCTGGC 20

RESULT 43
US-10-242-535A-23133/c
Sequence 23133, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: Chondrogene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
PRIOR FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23133
LENGTH: 400.
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (7)..(7)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (40)..(40)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (48)..(48)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (341)..(341)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
NAME/KEY: misc_feature
LOCATION: (394)..(394)
OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-23133

Query Match 85.6%; Score 15.4; DB 15; Length 400;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 CCGAAGGCACTCTGGC 18

DB 36 CCGAAGGCACTCTGGC 20

RESULT 44
US-09-922-217-755/c
Sequence 755, Application US/09922217
Patent No. US20020076414A1
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
APPLICANT: Jiang, Yugu
APPLICANT: Smith, Carole Lynn
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.471C13
CURRENT APPLICATION NUMBER: US/09/922,217
PRIOR FILING DATE: 2001-08-03
NUMBER OF SEQ ID NOS: 1124
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 755
LENGTH: 405
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 214, 305, 366, 368, 378
OTHER INFORMATION: n = A,T,C or G
US-09-922-217-755

Query Match 85.6%; Score 15.4; DB 9; Length 405;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 213 CCGAAGGCACTCTGGC 197

RESULT 45
US-09-833-263-755/c
Sequence 755, Application US/09833263
Patent No. US20020110547A1
GENERAL INFORMATION:
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Stolk, John A.
APPLICANT: Meagher, Madeleine J.
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
FILE REFERENCE: 210121.471C12
CURRENT APPLICATION NUMBER: US/09/833,263
PRIOR FILING DATE: 2001-04-10
NUMBER OF SEQ ID NOS: 1093
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 755
LENGTH: 405
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(405)
OTHER INFORMATION: n = A,T,C or G
US-09-833-263-755

Query Match 85.6%; Score 15.4; DB 9; Length 405;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTGGC 18
DB 213 CCGAAGGCACTGGC 197

RESULT 46

US-10-025-380-755/c
Sequence 755, Application US/10025380
Publication No. US20020182191A1

GENERAL INFORMATION:
APPLICANT: Xu, Jianshun
APPLICANT: Lodes, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Benson, Darin R.
APPLICANT: Meagher, Madeleine Joy
APPLICANT: Stolk, John A.
APPLICANT: Wang, Tongtong
APPLICANT: Jiang, Yugu
APPLICANT: Smith, Carole L.
APPLICANT: King, Gordon E.
APPLICANT: Wang, Aijun
APPLICANT: Clapper, Jonathan D.
APPLICANT: Fanger, Gary R.
APPLICANT: Vedyck, Thomas S.
APPLICANT: Carter, Darick
TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.471C14
CURRENT APPLICATION NUMBER: US/10/025.380
CURRENT FILING DATE: 2001-12-19
NUMBER OF SEQ ID NOS: 1129
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 755
LENGTH: 405
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 214, 305, 366, 368, 378
OTHER INFORMATION: n = A,T,C or G
US-10-025-380-755

Query Match 85.6%; Score 15.4; DB 13; Length 405;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTGGC 18
DB 213 CCGAAGGCACTGGC 197

RESULT 47

US-10-085-783A-58222/c
Sequence 58222, Application US/10085783A
Publication No. US20040037841A1

GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085.783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 58222
LENGTH: 422
TYPE: DNA
ORGANISM: Human

FEATURE:
NAME/KEY: misc_feature
LOCATION: (56)..(56)
OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-58222

Query Match 85.6%; Score 15.4; DB 12; Length 422;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTGGC 18
DB 305 CCGAAGGCACTGGC 289

RESULT 48

US-10-242-535A-58222/c
Sequence 58222, Application US/10242535A
Publication No. US20040013663A1

GENERAL INFORMATION:
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242.535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 58222
LENGTH: 422
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (56)..(56)
OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-58222

Query Match 85.6%; Score 15.4; DB 15; Length 422;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTGGC 18
DB 305 CCGAAGGCACTGGC 289

RESULT 49

US-10-085-783A-17255/c
Sequence 17255, Application US/10085783A
Publication No. US20040037841A1

GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085.783A
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340


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; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17255
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-17255

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Query Match      85.6%; Score 15.4; DB 12; Length 443;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      2 CCGAGAGGAGCTGTGGC 18
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Db      33 CCAGAGGAGCTGTGGC 17

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RESULT 50
US-10-242-535A-17255/c
; Sequence 17255, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17255
; LENGTH: 443
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-17255

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Query Match      85.6%; Score 15.4; DB 15; Length 443;
Best Local Similarity 94.1%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      2 CCGAGAGGAGCTGTGGC 18
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Db      33 CCAGAGGAGCTGTGGC 17

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Search completed: March 5, 2004, 02:19:51
Job time : 282 secs

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OM nucleic - nucleic search, using sw model

Run on: March 4, 2004, 23:56:01 ; Search time 80 Seconds
(without alignments)

124.864 Million cell updates/sec

Title: US-09-848-868-35

Perfect score: 18

Sequence: 1 cccggaagcagctctgc 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 27747546 residues 1365418

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	18	100.0	133	3	US-09-184-073-42
5	18	100.0	800	1	US-08-472-239-1
6	18	100.0	1070	3	US-09-414-436-4
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8	18	100.0	1307	1	US-08-047-041A-12
9	18	100.0	1317	1	US-07-912-011-1
10	18	100.0	1317	1	US-08-347-792-1
11	18	100.0	1317	1	US-08-431-357-1
12	18	100.0	1317	2	US-08-697-321-1
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16	18	100.0	1317	4	US-09-305-924-1
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18	18	100.0	1317	5	PCT-US95-15153-1
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22	15.4	85.6	447	4	US-09-614-124B-1634
23	15.4	85.6	447	4	US-09-671-325-1634
24	15.4	85.6	633	3	US-09-385-962-206
25	15.4	85.6	647	4	US-09-222-575-81
26	15.4	85.6	647	4	US-09-389-661-81
27	15.4	85.6	647	4	US-09-620-405B-81

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33	15	83.3	25	1	US-08-447-179-7	Sequence 7, Appl
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35	14.8	82.2	1757	3	US-08-094-071-1	Sequence 1, Appl
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37	14.8	82.2	8078	3	US-08-870-126-12	Sequence 12, Appl
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39	14.8	82.2	14985	1	US-08-652-972A-6	Sequence 6, Appl
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47	14.4	80.0	982	1	US-08-466-127-1	Sequence 7, Appl
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59	13.8	76.7	579	4	US-09-215-681-188	Sequence 188, Appl
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61	13.8	76.7	584	4	US-09-404-879A-187	Sequence 187, Appl
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66	13.8	76.7	630	1	US-08-527-327A-5	Sequence 5, Appl
67	13.8	76.7	655	4	US-09-643-597-208	Sequence 208, Appl
68	13.8	76.7	655	4	US-09-480-884A-208	Sequence 208, Appl
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82	13.8	76.7	1001	4	US-09-671-317-231	Sequence 231, Appl
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87	13.8	76.7	1365	4	US-09-489-039A-499	Sequence 499, Appl
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C 103	13.8	76.7	1665	4	US-09-252-991A-10272	Sequence 10272, A
C 104	13.8	76.7	1716	2	US-08-954-333-9	Sequence 9, Appl
C 105	13.8	76.7	1816	1	US-08-539-666-3	Sequence 3, Appl
C 106	13.8	76.7	1817	1	US-07-612-673-3	Sequence 3, Appl
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C 115	13.8	76.7	3519	1	US-08-485-618-45	Sequence 45, Appl
C 116	13.8	76.7	3519	1	US-08-362-652-45	Sequence 45, Appl
C 117	13.8	76.7	3519	1	US-08-605-672-45	Sequence 45, Appl
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C 169	13.4	74.4	417	4	US-09-216-393B-15	Sequence 15, Appl
C 170	13.4	74.4	459	4	US-09-621-976-3407	Sequence 3407, Ap
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C 173	13.4	74.4	601	4	US-09-814-951A-11	Sequence 11, Appl

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C 199 13.4 74.4 33000 4 US-09-215-694-18 Sequence 18, Appl

C 200 13.2 73.3 21 4 US-09-632-675-8 Sequence 8, Appl

RESULT 1

US-08-047-041A-15/C

Sequence 15, Application US/08047041A

Patent No. 5527676

GENERAL INFORMATION:

APPLICANT: Vogelstein, Bert

APPLICANT: Baker, Suzanne J.

APPLICANT: Fearon, Eric R.

APPLICANT: Nigro, Janice M.

TITLE OF INVENTION: Detection of Loss of the wild-type p53

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSER: Banner & Allegretti, Ltd.

STREET: 1001 G Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20001.4597

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/047,041A

FILING DATE: 22-MAR-1993

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/928,661

FILING DATE: 17-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/446,584

FILING DATE: 06-DEC-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/330,566

FILING DATE: 29-MAR-1989

ATTORNEY/AGENT INFORMATION:

NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141

REFERENCE/DOCKET NUMBER: 0107.42917

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: exon 2
PUBLICATION INFORMATION:
AUTHORS: Lamb,
JOURNAL: Mol. Cell. Biol.
VOLUME: 6
ISSUE: 5
PAGES: 1379-1385
DATE: 1986
US-08-047-041A-15

Query Match 100.0%; Score 18; DB 1; Length 102;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGAGGCGAGTCTGGC 18
Db 20 CCGGAGGCGAGTCTGGC 3

RESULT 2
US-08-047-041A-2/c
Sequence 2, Application US/08047041A
Patent No. 5527676
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Pearson, Eric R.
TITLE OF INVENTION: Detection of loss of the wild-type p53
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allgretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001, 4597
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047,041A
FILING DATE: 22-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446,584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.

REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42917
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
CHROMOSOME/SEGMENT: exon 2
PUBLICATION INFORMATION:
AUTHORS: Buchman, V. L.
TITLE: A variation in the structure of the
TITLE: protein-coding region of the human p53 gene
JOURNAL: Gene
VOLUME: 70
PAGES: 245-252
DATE: 1988
US-08-047-041A-2

Query Match 100.0%; Score 18; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGAGGCGAGTCTGGC 18
Db 35 CCGGAGGCGAGTCTGGC 18

RESULT 3
US-08-795-006A-22/c
Sequence 22, Application US/08795006A
Patent No. 5840579
GENERAL INFORMATION:
APPLICANT: Boeke, Jef
APPLICANT: Brachmann, Rainer
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING P53
TITLE OF INVENTION: MUTATIONS WHICH SUPPRESS P53 CANCER MUTATIONS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,006A
FILING DATE: 05-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.03170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-795-006A-22

Query Match 100.0%; Score 18; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCGAGTCTGGC 18
DB 35 CCCGGAAGGCGAGTCTGGC 18

RESULT 4
US-09-184-073-22/c
Sequence 22, Application US/09184073

PATENT No. 6183964
GENERAL INFORMATION:
APPLICANT: Boeke, Jef
ATTORNEY/AGENT INFORMATION:
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING P53
TITLE OF INVENTION: MUTATIONS WHICH SUPPRESS P53 CANCER MOTA- TIONS
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESSES:
ADDRESS: Banner & Witcoff
STREET: 1001 G Street, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20001

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/184,073
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/795,006
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107,03170
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX:

INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-184-073-22

Query Match 100.0%; Score 18; DB 3; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCGAGTCTGGC 18
DB 35 CCCGGAAGGCGAGTCTGGC 18

RESULT 5
US-08-472-239-1/c
Sequence 1, Application US/08472239

PATENT No. 5728526
GENERAL INFORMATION:
APPLICANT: GEORGE, Jr., Albert L.
APPLICANT: BHATNAGAR, Satish K.
APPLICANT: NAZARENKO, Irena
TITLE OF INVENTION: METHOD FOR ANALYZING A NUCLEOTIDE
TITLE OF INVENTION: SEQUENCE AND KIT THEREFOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESSES:
ADDRESS: BURNS, DOANE, SWECKER & MATSIS
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,239
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mukai, Robert G.
REGISTRATION NUMBER: 28,531
REFERENCE/DOCKET NUMBER: 020160-229
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 800 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-472-239-1

Query Match 100.0%; Score 18; DB 1; Length 800;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGCGAGTCTGGC 18
DB 108 CCCGGAAGGCGAGTCTGGC 91

RESULT 6
US-09-414-436-4/c
Sequence 4, Application US/09414436

PATENT No. 6294384
GENERAL INFORMATION:
APPLICANT: Dell'Acqua, Giorgio
APPLICANT: Mann, Michael J.
APPLICANT: Dzaui, Victor J.
TITLE OF INVENTION: Compositions and Methods Based Upon an Isoform of p53
FILE REFERENCE: p53f
CURRENT APPLICATION NUMBER: US/09/414,436
CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: 60/103,849
EARLIER FILING DATE: 1999-10-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 4
LENGTH: 1070
TYPE: DNA
ORGANISM: Homo sapiens
US-09-414-436-4

Query Match 100.0%; Score 18; DB 3; Length 1070;
Best Local Similarity 100.0%; Pred. No. 4.3;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGAGGAGCTGGC 18
Db 127 CCGGAGGAGCTGGC 110

RESULT 7

US-08-047-041A-13/C
Sequence 13, Application US/08047041A
Patent No. 5527676
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detection of loss of the wild-type p53
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001.4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047, 041A
FILING DATE: 22-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446,584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42917
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1303 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
MAP POSITION: 17p13.1
PUBLICATION INFORMATION:
AUTHORS: Harris, N.
JOURNAL: Mol. Cell. Biol.
VOLUME: 6
ISSUE: 12
PAGES: 4650-4656
DATE: 1986
US-08-047-041A-13

Query Match 100.0%; Score 18; DB 1; Length 1303;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGGAGGAGCTGGC 18
Db 113 CCGGAGGAGCTGGC 96

RESULT 8

US-08-047-041A-12/C
Sequence 12, Application US/08047041A
Patent No. 5527676
GENERAL INFORMATION:
APPLICANT: Vogelstein, Bert
APPLICANT: Baker, Suzanne J.
APPLICANT: Fearon, Eric R.
APPLICANT: Nigro, Janice M.
TITLE OF INVENTION: Detection of loss of the wild-type p53
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Allegretti, Ltd.
STREET: 1001 G Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20001.4597
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/047, 041A
FILING DATE: 22-MAR-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/928,661
FILING DATE: 17-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/446,584
FILING DATE: 06-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/330,566
FILING DATE: 29-MAR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 01107.42917
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1307 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
POSITION IN GENOME:
MAP POSITION: 17p13.1
PUBLICATION INFORMATION:
AUTHORS: Harris, N.
TITLE: Molecular basis for heterogeneity of the
TITLE: human p53 protein
JOURNAL: Mol. Cell. Biol.
VOLUME: 6
ISSUE: 12

PAGES: 4650-4656
DATE: 1986
US-08-047-041A-12

Query Match 100.0%; Score 18; DB 1; Length 1307;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGAGCTCTGGC 18
|||||
DB 117 CCCGGAAGGAGCTCTGGC 100

RESULT 9
US-07-912-011-1/C

Sequence 1, Application US/07912011
Patent No. 5382510

GENERAL INFORMATION:

APPLICANT: Levine, Arnold J.

APPLICANT: Shenk, Thomas E.

APPLICANT: Finlay, Cathy A.

TITLE OF INVENTION: Probes for Detecting Mutant p53

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:

ADDRESSEE: Imclone Systems Incorporated

STREET: 180 Varick Street

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10014

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/912.011

FILING DATE: 10-JUL-1992

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Felt, Irving N.

REGISTRATION NUMBER: 28, 601

REFERENCE/DOCKET NUMBER: LEV-1-C

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-645-1405

TELEFAX: 212-645-2054

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1317 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-07-912-011-1

Query Match 100.0%; Score 18; DB 1; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGAGCTCTGGC 18
|||||
DB 127 CCCGGAAGGAGCTCTGGC 110

RESULT 10
US-08-347-792-1/C

Sequence 1, Application US/08347792
Patent No. 5573925

GENERAL INFORMATION:

APPLICANT: Halazonetis, Thomas D.

TITLE OF INVENTION: p53 Proteins With Altered

Tetramerization Domains

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr., PO Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/347,792

FILING DATE:

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.

REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: MST58USA

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9206

TELEFAX: 215-540-5818

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1317 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 136..1314

US-08-347-792-1

Query Match 100.0%; Score 18; DB 1; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGGAAGGAGCTCTGGC 18
|||||
DB 127 CCCGGAAGGAGCTCTGGC 110

RESULT 11
US-08-431-357-1/C

Sequence 1, Application US/08431357
Patent No. 5721340

GENERAL INFORMATION:

APPLICANT: Halazonetis, Thomas D.

TITLE OF INVENTION: p53 Proteins With Altered

Tetramerization Domains

NUMBER OF SEQUENCES: 37

CORRESPONDENCE ADDRESS:

ADDRESSEE: Howson and Howson

STREET: Spring House Corporate Cntr., PO Box 457

CITY: Spring House

STATE: Pennsylvania

COUNTRY: USA

ZIP: 19477

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/431,357

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/347,792

FILING DATE: 28-NOV-1994

ATTORNEY/AGENT INFORMATION:

NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST580USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1314
US-08-431-357-1

Query Match 100.0%; Score 18; DB 1; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGAAGGCGAGTCTGGC 18
Db 127 CCCGGAAGGCGAGTCTGGC 110

RESULT 12
US-08-697-221-1/c
Sequence 1, Application US/08697221
Patent No. 5847083
GENERAL INFORMATION:
APPLICANT: Halazoneitis, Thanos D.
TITLE OF INVENTION: Modified p53 Constructs and Uses
TITLE OF INVENTION: Therefor
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 15477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/697,221
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,802
FILING DATE: 22-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kodroff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: WST64AUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1314
US-08-697-221-1

Query Match 100.0%; Score 18; DB 2; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGAAGGCGAGTCTGGC 18
Db 127 CCCGGAAGGCGAGTCTGGC 110

RESULT 13
US-08-392-542-1/c
Sequence 1, Application US/08392542
Patent No. 6169073
GENERAL INFORMATION:
APPLICANT: Halazoneitis, Thanos
TITLE OF INVENTION: Peptides and peptidomimetics with
STRUCTURAL SIMILARITY TO HUMAN P53
TITLE OF INVENTION: Function
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,542
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 0486.48439
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-392-542-1

Query Match 100.0%; Score 18; DB 3; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCGGAAGGCGAGTCTGGC 18
Db 127 CCCGGAAGGCGAGTCTGGC 110

RESULT 14
US-08-894-327-1/c
Sequence 1, Application US/08894327
Patent No. 6245886
GENERAL INFORMATION:
APPLICANT: Halazoneitis, Thanos
TITLE OF INVENTION: Peptides and peptidomimetics with
STRUCTURAL SIMILARITY TO HUMAN P53 THAT ACTIVATE P53
TITLE OF INVENTION: structural similarity to human p53 that activate p53

TITLE OF INVENTION: function
FILE REFERENCE: 2973.1998
CURRENT APPLICATION NUMBER: US/08/894,327
CURRENT FILING DATE: 1997-12-04
EARLIER APPLICATION NUMBER: pctus96/01335
EARLIER FILING DATE: 1996-02-16
EARLIER APPLICATION NUMBER: 08/392,542
EARLIER FILING DATE: 1995-02-16
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1317
TYPE: DNA
ORGANISM: Homo sapiens
US-08-894-327-1

Query Match 100.0%; Score 18; DB 3; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTCTGGC 18
DB 127 CCCGAGAGCAGCTCTGGC 110

RESULT 15
US-09-147-751-8/c
Sequence 8, Application US/09147751
Patent No. 6335164
GENERAL INFORMATION:
APPLICANT: KIGAWA, Koji
APPLICANT: YAMANAKA, Mikayo
APPLICANT: KUSUMI, Kayo
APPLICANT: MUKAI, Eiji
APPLICANT: OBARA, Kazuaki
TITLE OF INVENTION: METHODS FOR TARGETING, ENRICHING,
TITLE OF INVENTION: DETECTING AND/OR ISOLATING TARGET NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: USING RECA-LIKE RECOMBINASE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FOLSY & LARDNER
STREET: 3000 K Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/147,751
FILING DATE: 18-MAY-1999
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/JP97/03019
FILING DATE: 23-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8/347090
FILING DATE: 26-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8/229061
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Maebius, Stephen B.
REGISTRATION NUMBER: 35,264
REFERENCE/DOCKET NUMBER: 84335/108
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:

LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
US-09-147-751-8

Query Match 100.0%; Score 18; DB 4; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTCTGGC 18
DB 127 CCCGAGAGCAGCTCTGGC 110

RESULT 16
US-09-305-914-1/c
Sequence 1, Application US/09305914
Patent No. 6388062
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos D.
APPLICANT: Stavridi, Elena S.
TITLE OF INVENTION: Modified p53 Tetramerization Domains Having Hydrophobic
TITLE OF INVENTION: Amino Acid Substitutions
FILE REFERENCE: W8784AUSA
CURRENT APPLICATION NUMBER: US/09/305,914
CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: 60/084,839
EARLIER FILING DATE: 1998-05-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1317
TYPE: DNA
ORGANISM: human p53
FEATURE:
NAME/KEY: CDS
LOCATION: (136)..(1314)
US-09-305-914-1

Query Match 100.0%; Score 18; DB 4; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCGAGAGCAGCTCTGGC 18
DB 127 CCCGAGAGCAGCTCTGGC 110

RESULT 17
US-09-685-027-1/c
Sequence 1, Application US/09685027
Patent No. 6420118
GENERAL INFORMATION:
APPLICANT: Halazonetis, Thanos
APPLICANT: Hartwig, Wolfgang
TITLE OF INVENTION: Peptides and Peptidomimetics with
Structural Similarity to Human p53 That Activate p53
Function
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/685,027
FILING DATE: 10-OCT-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/392,542
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 0486,48439
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-685-027-1

Query Match 100.0%; Score 18; DB 4; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCGGAGGCGAGTCTGGC 18
Db 127 CCGGAGGCGAGTCTGGC 110

RESULT 18
PCT-US95-15353-1/c
Sequence 1, Application PC/TUS9515353
GENERAL INFORMATION:
APPLICANT: The Wistar Institute of Anatomy
APPLICANT: and Biology
APPLICANT: Halazonetis, Thanos D.
TITLE OF INVENTION: p53 Proteins With Altered
TITLE OF INVENTION: Tetramerization Domains
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr., PO Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15353
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/347,792
FILING DATE: 28-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/431,357
FILING DATE: 28-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/456,623
FILING DATE: 01-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: WST586CPT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9206
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 136..1314
PCT-US95-15353-1

Query Match 100.0%; Score 18; DB 5; Length 1317;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCGGAGGCGAGTCTGGC 18
Db 127 CCGGAGGCGAGTCTGGC 110

RESULT 19
US-09-404-879A-332
Sequence 332, Application US/09404879A
Patent No. 6468946
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 332
LENGTH: 184
TYPE: DNA
ORGANISM: Homo sapiens
US-09-404-879A-332

Query Match 85.6%; Score 15.4; DB 4; Length 184;
Best Local Similarity 94.1%; Pred. No. 7.4;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 CCGGAGGCGAGTCTGGC 18
Db 112 CCGGAGGCGAGTCTGGC 128

RESULT 20
US-09-702-705-1634/c
Sequence 1634, Application US/09702705
Patent No. 6504010
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Vedvick, Tom
APPLICANT: Carter, Darick
APPLICANT: Retter, Marc
APPLICANT: Mannion, Jane
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C14
CURRENT APPLICATION NUMBER: US/09/702,705

;; CURRENT FILING DATE: 2000-10-30
;; NUMBER OF SEQ ID NOS: 1833
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 1634
;; LENGTH: 447
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-702-705-1634

Query Match 85.6%; Score 15.4; DB 4; Length 447;
Best Local Similarity 94.1%; Pred. No. 78;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 73 CCGAAGGCACTCTGGC 57

RESULT 21
US-09-736-457-1634/c
;; Sequence 1634, Application US/09736457
;; Patent No. 6509448
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Tonglong
;; APPLICANT: Bangur, Chaitanya S.
;; APPLICANT: Lodes, Michael A.
;; APPLICANT: Fanger, Gary
;; APPLICANT: Vedvick, Tom
;; APPLICANT: Carter, Darick
;; APPLICANT: Retter, Marc
;; APPLICANT: Mannion, Jane
;; APPLICANT: Fan, Liqun
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;; FILE REFERENCE: 210121.478C15
;; CURRENT APPLICATION NUMBER: US/09/736,457
;; CURRENT FILING DATE: 2000-12-13
;; NUMBER OF SEQ ID NOS: 1864
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 1634
;; LENGTH: 447
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-736-457-1634

Query Match 85.6%; Score 15.4; DB 4; Length 447;
Best Local Similarity 94.1%; Pred. No. 78;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 73 CCGAAGGCACTCTGGC 57

RESULT 22
US-09-614-124B-1634/c
;; Sequence 1634, Application US/09614124B
;; Patent No. 6630574
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Tonglong
;; APPLICANT: Bangur, Chaitanya S.
;; APPLICANT: Lodes, Michael A.
;; APPLICANT: Fanger, Gary
;; APPLICANT: Vedvick, Tom
;; APPLICANT: Carter, Darick
;; APPLICANT: Retter, Marc
;; APPLICANT: Mannion, Jane
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
;; FILE REFERENCE: 210121.478C9
;; CURRENT APPLICATION NUMBER: US/09/614,124B
;; CURRENT FILING DATE: 2001-07-11

;; NUMBER OF SEQ ID NOS: 1668
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 1634
;; LENGTH: 447
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-614-124B-1634

Query Match 85.6%; Score 15.4; DB 4; Length 447;
Best Local Similarity 94.1%; Pred. No. 78;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 73 CCGAAGGCACTCTGGC 57

RESULT 23
US-09-671-325-1634/c
;; Sequence 1634, Application US/09671325
;; Patent No. 6667154
;; GENERAL INFORMATION:
;; APPLICANT: Wang, Tonglong
;; APPLICANT: Bangur, Chaitanya S.
;; APPLICANT: Lodes, Michael A.
;; APPLICANT: Fanger, Gary
;; APPLICANT: Vedvick, Tom
;; APPLICANT: Carter, Darick
;; APPLICANT: Retter, Marc
;; APPLICANT: Mannion, Jane
;; APPLICANT: Fan, Liqun
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
;; FILE REFERENCE: 210121.478C12
;; CURRENT APPLICATION NUMBER: US/09/671,325
;; CURRENT FILING DATE: 2000-09-26
;; NUMBER OF SEQ ID NOS: 1825
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 1634
;; LENGTH: 447
;; TYPE: DNA
;; ORGANISM: Homo sapiens
US-09-671-325-1634

Query Match 85.6%; Score 15.4; DB 4; Length 447;
Best Local Similarity 94.1%; Pred. No. 78;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
DB 73 CCGAAGGCACTCTGGC 57

RESULT 24
US-09-385-982-206/c
;; Sequence 206, Application US/09385982
;; Patent No. 6262334
;; GENERAL INFORMATION:
;; APPLICANT: ENDEGE, WILSON O., ET AL.
;; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
;; FILE REFERENCE: CCDNA-260XX
;; CURRENT APPLICATION NUMBER: US/09/385,982
;; CURRENT FILING DATE: 1999-08-30
;; EARLIER APPLICATION NUMBER: 09/328,111
;; EARLIER FILING DATE: 1999-06-08
;; EARLIER APPLICATION NUMBER: 60/117,393
;; EARLIER FILING DATE: 1999-01-27
;; EARLIER APPLICATION NUMBER: 60/098,639
;; EARLIER FILING DATE: 1998-08-31
;; NUMBER OF SEQ ID NOS: 544
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 206

LENGTH: 633
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(633)
OTHER INFORMATION: n = A,T,C or G
US-09-385-982-206

Query Match 85.6%; Score 15.4; DB 3; Length 633;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
|||
DB 426 CCGAAGGCACTCTGGC 410

RESULT 25
US-09-222-575-81
Sequence 81, Application US/09222575
Patent No. 6387697
GENERAL INFORMATION:
APPLICANT: Yugui, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: Compositions for the Treatment and Diagnosis of Breast Cancer
FILE REFERENCE: 210121.470
CURRENT APPLICATION NUMBER: US/09/222,575
CURRENT FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 174
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 81
LENGTH: 647
TYPE: DNA
ORGANISM: Human
US-09-222-575-81

Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
|||
DB 575 CCGAAGGCACTCTGGC 591

RESULT 26
US-09-389-681-81
Sequence 81, Application US/09389681A
Patent No. 6518237
GENERAL INFORMATION:
APPLICANT: Yugui, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.470C3
CURRENT APPLICATION NUMBER: US/09/389,681A
CURRENT FILING DATE: 1999-09-02
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 81
LENGTH: 647
TYPE: DNA
ORGANISM: Homo sapien
US-09-389-681-81

Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
|||
DB 575 CCGAAGGCACTCTGGC 591

RESULT 27
US-09-620-405B-81
Sequence 81, Application US/09620405B
Patent No. 6528054
GENERAL INFORMATION:
APPLICANT: Jiang, Yugui
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
APPLICANT: Harlocker, Susan L.
APPLICANT: Hepler, William T.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
FILE REFERENCE: 210121.470C8
CURRENT APPLICATION NUMBER: US/09/620,405B
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 495
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 81
LENGTH: 647
TYPE: DNA
ORGANISM: Homo sapien
US-09-620-405B-81

Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
|||
DB 575 CCGAAGGCACTCTGGC 591

RESULT 28
US-09-339-338-81
Sequence 81, Application US/09339338A
Patent No. 6573368
GENERAL INFORMATION:
APPLICANT: Yugui, Jiang
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Xu, Jiangchun
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121.470C2
CURRENT APPLICATION NUMBER: US/09/339,338A
CURRENT FILING DATE: 1999-06-23
NUMBER OF SEQ ID NOS: 315
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 81
LENGTH: 647
TYPE: DNA
ORGANISM: Homo sapien
US-09-339-338-81

Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCACTCTGGC 18
|||
DB 575 CCGAAGGCACTCTGGC 591

RESULT 29
US-09-433-826B-81

; Sequence 81, Application US/09433826B
; Patent No. 6579973
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqi
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C4
; CURRENT APPLICATION NUMBER: US/09/433,826B
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 474
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-433-826B-81

Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCGAGTCTGGC 18
|||
Db 575 CCAGAAGCGAGTCTGGC 591

RESULT 30
US-09-604-287A-81
; Sequence 81, Application US/09604287A
; Patent No. 6586572
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqi
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C7
; CURRENT APPLICATION NUMBER: US/09/604,287A
; CURRENT FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 489
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-604-287A-81

Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCGAGTCTGGC 18
|||
Db 575 CCAGAAGCGAGTCTGGC 591

RESULT 31
US-09-285-480-81
; Sequence 81, Application US/09285480
; Patent No. 6590076
; GENERAL INFORMATION:
; APPLICANT: Yuqi, Jiang
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND

; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.470C1
; CURRENT APPLICATION NUMBER: US/09/285,480
; CURRENT FILING DATE: 1999-04-02
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-285-480-81

Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCGAGTCTGGC 18
|||
Db 575 CCAGAAGCGAGTCTGGC 591

RESULT 32
US-09-834-759-81
; Sequence 81, Application US/09834759
; Patent No. 6680197
; GENERAL INFORMATION:
; APPLICANT: Jiang, Yuqi
; APPLICANT: Dillon, Devin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Xu, Jiangchun
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Hepler, William T.
; APPLICANT: Henderson, Robert A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.470C9
; CURRENT APPLICATION NUMBER: US/09/834,759
; CURRENT FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 547
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-834-759-81

Query Match 85.6%; Score 15.4; DB 4; Length 647;
Best Local Similarity 94.1%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 CCGAAGGCGAGTCTGGC 18
|||
Db 575 CCAGAAGCGAGTCTGGC 591

RESULT 33
US-08-447-179-7/C
; Sequence 7, Application US/08447179
; Patent No. 5744303
; GENERAL INFORMATION:
; APPLICANT: Isgo, Richard
; APPLICANT: Friend, Stephen H.
; APPLICANT: Prebourg, Thierry
; APPLICANT: Ishioka, Chikashi
; TITLE OF INVENTION: FUNCTIONAL ASSAY FOR TUMOR
; TITLE OF INVENTION: SUPPRESSOR GENES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.

ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,179
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/046,033
FILING DATE: 12 APRIL 1993
APPLICATION NUMBER: 07/956,696
FILING DATE: 10 OCTOBER 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/159002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 25
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-447-179-7

Query Match 83.3%; Score 15; DB 1; Length 25;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGAAGCAGCTGCGC 18
DB 23 GGAAGCAGCTGCGC 11

RESULT 34
US-09-445-247-21/c
Sequence 21, Application US/09445247
Patent No. 6410238
GENERAL INFORMATION:
APPLICANT: Wistar Institute of Anatomy & Biology
Sakamuro, Daitoku
PREDECESSOR: George C.
TITLE OF INVENTION: Box-Dependent MYC-Interacting Protein
(Bmi1) Compositions and Uses Therefor
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/445,247
FILING DATE: 03-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/870,126
FILING DATE: 06-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215

REFERENCE/DOCKET NUMBER: WST6D0PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 108 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..108
SEQUENCE DESCRIPTION: SEQ ID NO: 21:
US-09-445-247-21

Query Match 82.2%; Score 14.8; DB 4; Length 108;
Best Local Similarity 88.9%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGCGC 18
DB 36 CCCGGAAGCAGCTGCGC 19

RESULT 35
US-08-094-071-1/c
Sequence 1, Application US/08094071
Patent No. 6083709
GENERAL INFORMATION:
APPLICANT: Reynolds, Frederick H.
APPLICANT: Sorvillo, John M.
APPLICANT: Zehab, Ron J.
APPLICANT: Stephenson, John R.
TITLE OF INVENTION: Immunoassay for Detection of
TITLE OF INVENTION: mutant p53 polypeptide in
TITLE OF INVENTION: biological fluids
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/094,071
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 719,172
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 649,566
FILING DATE: 01-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 298,776
FILING DATE: 17-JAN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 298,837
FILING DATE: 18-JAN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 885,627
FILING DATE: 23-JUL-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 767,862
FILING DATE: 21-AUG-1985

PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU 61540/86
FILING DATE: 18-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CA 516,260
FILING DATE: 19-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 86,111 527.7
FILING DATE: 20-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 195121/86
FILING DATE: 20-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NZ 217,209
FILING DATE: 14-AUG-1986
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 23384-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 coop ul
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
IMMEDIATE SOURCE:
CLONE: activated p53 oncogene
PUBLICATION INFORMATION:
AUTHORS: Harlow, E.
AUTHORS: Williamson, N. M.
AUTHORS: Ralston, R.
AUTHORS: Helfman, D. M.
AUTHORS: Adams, T. E.
TITLE: Molecular Cloning and In-Vitro
TITLE: Expression of a C-DNA Clone for Human
TITLE: Cellular Tumor Antigen P53
JOURNAL: Molecular and Cellular Biology
VOLUME: 5
ISSUE: 7
PAGES: 1601-1610
DATE: July-1985
US-08-094-071-1

Query Match 82.2%; Score 14.8; DB 3; Length 1757;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGGAAGGCGAGCTGGC 18
DB 206 CCGGAAGGCGAGCTGGC 189

RESULT 36
PCT-US92-00878-1/C
Sequence 1, Application PC/TUS9200878
GENERAL INFORMATION:
APPLICANT: Reynolds, Frederick H.
APPLICANT: Scivillio, John M.
APPLICANT: Zehnb, Ron J.
APPLICANT: Stephenson, John R.
TITLE OF INVENTION: Immunoassay for Detection of mutant p53
TITLE OF INVENTION: polypeptide in biological fluids
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper and Dunham
STREET: 30 Rockefeller Plaza

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/00878
FILING DATE: 19920131
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 719,172
FILING DATE: 21-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 649,566
FILING DATE: 01-FEB-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 298,776
FILING DATE: 17-JAN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 298,837
FILING DATE: 18-JAN-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 885,627
FILING DATE: 23-JUL-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 767,862
FILING DATE: 21-AUG-1985
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU 61540/86
FILING DATE: 18-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CA 516,260
FILING DATE: 19-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 86,111 527.7
FILING DATE: 20-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 195121/86
FILING DATE: 20-AUG-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NZ 217,209
FILING DATE: 14-AUG-1986
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 23384-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 664-0525
TELEX: 422523 coop ul
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1757 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: N
ANTI-SENSE: N
IMMEDIATE SOURCE:
CLONE: activated p53 oncogene
PUBLICATION INFORMATION:
AUTHORS: Harlow, E.
AUTHORS: Williamson, N. M.
AUTHORS: Ralston, R.
AUTHORS: Helfman, D. M.
AUTHORS: Adams, T. E.
TITLE: Molecular Cloning and In-Vitro Expression of a C-DNA
TITLE: Clone for Human Cellular Tumor Antigen P53

JOURNAL: Molecular and Cellular Biology
VOLUME: 5
ISSUE: 7
PAGES: 1601-1610
DATE: July-1985
PCT-US92-00878-1

Query Match 82.2%; Score 14.8; DB 5; Length 1757;
Best Local Similarity 88.9%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGGAAGCAGCTGGC 18
Db CCGGAAGCAGCTGGC 189

RESULT 37
US-08-870-126-12/c
Sequence 12, Application US/08870126
Patent No. 6048702
GENERAL INFORMATION:
APPLICANT: Pendergast, George C.
TITLE OF INVENTION: Murine and Human Box-Dependent
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/870,126
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,454
FILING DATE: 05-MAY-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/652,972
FILING DATE: 24-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kodroff, Cathy A.
REGISTRATION NUMBER: 33,980
REFERENCE/DOCKET NUMBER: WST60CUSA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8078 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: exon
LOCATION: 1841..1948
OTHER INFORMATION: /note= "putative.alt.exon"
FEATURE:
NAME/KEY: exon
LOCATION: 2409..2432
OTHER INFORMATION: /note= "putative.alt.exon"
FEATURE:
NAME/KEY: exon
LOCATION: 3308..3601

OTHER INFORMATION: /note= "putative.alt.exon"
FEATURE:
NAME/KEY: exon
LOCATION: 4613..4702
OTHER INFORMATION: /note= "exon 13"
FEATURE:
NAME/KEY: exon
LOCATION: 4944..5054
OTHER INFORMATION: /note= "exon 14"
FEATURE:
NAME/KEY: exon
LOCATION: 5334..5435
OTHER INFORMATION: /note= "exon 15"
FEATURE:
NAME/KEY: exon
LOCATION: 7223..7783
OTHER INFORMATION: /note= "exon 16"
US-08-870-126-12

Query Match 82.2%; Score 14.8; DB 3; Length 8078;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGGAAGCAGCTGGC 18
Db 3529 CCGGAAGCAGCTGGC 3512

RESULT 38
US-09-445-247-12/c
Sequence 12, Application US/09445247
Patent No. 6410238
GENERAL INFORMATION:
APPLICANT: Wistar Institute of Anatomy & Biology
Pendergast, George C.
TITLE OF INVENTION: Box-Dependent MYC-Interacting Protein
(Bin1) Compositions and Uses Therefor
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESS: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/445,247
FILING DATE: 03-Dec-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/870,126
FILING DATE: 06-JUN-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST60DPCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8078 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE:

NAME/KEY: exon
LOCATION: 1841..1948
OTHER INFORMATION: /note= "exon 12B"
FEATURE: NAME/KEY: exon
LOCATION: 2409..2432
OTHER INFORMATION: /note= "exon 12C"
FEATURE: NAME/KEY: exon
LOCATION: 3494..3601
OTHER INFORMATION: /note= "exon 12D"
FEATURE: NAME/KEY: exon
LOCATION: 4613..4702
OTHER INFORMATION: /note= "exon 13"
FEATURE: NAME/KEY: exon
LOCATION: 4944..5054
OTHER INFORMATION: /note= "exon 14"
FEATURE: NAME/KEY: exon
LOCATION: 5334..5435
OTHER INFORMATION: /note= "exon 15"
FEATURE: NAME/KEY: exon
LOCATION: 7223..7783
OTHER INFORMATION: /note= "exon 16"
SEQUENCE DESCRIPTION: SEQ ID NO: 12;
US-09-445-247-12

Query Match 82.2%; Score 14.8; DB 4; Length 8078;
Best Local Similarity 88.9%; Pred. No. 1.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGCGC 18
DB 3529 CCCGGAAGCAGCGCTGCC 3512

RESULT 39
US-08-652-972A-6/c
Sequence 6, Application US/08652972A
Patent No. 5723581
GENERAL INFORMATION:
APPLICANT: Prendergast, George C.
APPLICANT: Sakamuro, Daitoku
TITLE OF INVENTION: Murine and Human Box-Dependent
TITLE OF INVENTION: MYC-Interacting Protein (BIN1) and Uses Therefor
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howson and Howson
STREET: Spring House Corporate Cntr, P O Box 457
CITY: Spring House
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19477
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,972A
FILING DATE: 24-MAY-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,454
FILING DATE: 05-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bak, Mary E.
REGISTRATION NUMBER: 31,215
REFERENCE/DOCKET NUMBER: WST608BUSA
TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-540-9200
TELEFAX: 215-540-5818
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 14985 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
FEATURE: NAME/KEY: unsure
LOCATION: 1332
OTHER INFORMATION: /note= "unsequenced segment"
FEATURE: NAME/KEY: unsure
LOCATION: 3225
OTHER INFORMATION: /note= "unsequenced segment"
FEATURE: NAME/KEY: unsure
LOCATION: 7209
OTHER INFORMATION: /note= "unsequenced segment"
FEATURE: NAME/KEY: unsure
LOCATION: 11097
OTHER INFORMATION: /note= "unsequenced segment"
FEATURE: NAME/KEY: exon
LOCATION: 1..324
OTHER INFORMATION: /note= "Exon 1"
FEATURE: NAME/KEY: exon
LOCATION: 325..1618
OTHER INFORMATION: /note= "Exon 2"
FEATURE: NAME/KEY: exon
LOCATION: 1619..3174
OTHER INFORMATION: /note= "Exon 3"
FEATURE: NAME/KEY: exon
LOCATION: 3175..4365
OTHER INFORMATION: /note= "Exon 4"
FEATURE: NAME/KEY: exon
LOCATION: 4441..11518
OTHER INFORMATION: /note= "Exon 5"
FEATURE: NAME/KEY: exon
LOCATION: 11519..11850
OTHER INFORMATION: /note= "Exon 6"
FEATURE: NAME/KEY: exon
LOCATION: 11851..12240
OTHER INFORMATION: /note= "Exon 7"
FEATURE: NAME/KEY: exon
LOCATION: 12241..14129
OTHER INFORMATION: /note= "Exon 8"
FEATURE: NAME/KEY: exon
LOCATION: 14130..14985
OTHER INFORMATION: /note= "Exon 9"
US-08-652-972A-6

Query Match 82.2%; Score 14.8; DB 1; Length 14985;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCGGAAGCAGCTGCGC 18
DB 10738 CCCGGAAGCAGCGCTGCC 10721

RESULT 40

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PCT-US96-06231A-6/c
; Sequence 6, Application PC/TUS9606231A
; GENERAL INFORMATION:
; APPLICANT: Wistar Institute of Anatomy & Biology
; TITLE OF INVENTION: Murine and Human Box-Dependent
; and Uses Therefor
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr, P O Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/06231A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,454
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WST60APCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9200
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14985 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 1332
; OTHER INFORMATION: /note= "unsequenced segment"
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 3225
; OTHER INFORMATION: /note= "unsequenced segment"
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 7209
; OTHER INFORMATION: /note= "unsequenced segment"
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 11097
; OTHER INFORMATION: /note= "unsequenced segment"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1..324
; OTHER INFORMATION: /note= "Exon 1"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 325..1618
; OTHER INFORMATION: /note= "Exon 2"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1619..3174
; OTHER INFORMATION: /note= "Exon 3"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3175..4365
; OTHER INFORMATION: /note= "Exon 4"
; FEATURE:

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; NAME/KEY: exon
; LOCATION: 4441..11518
; OTHER INFORMATION: /note= "Exon 5"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 11519..11850
; OTHER INFORMATION: /note= "Exon 6"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 11851..12240
; OTHER INFORMATION: /note= "Exon 7"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 12241..14129
; OTHER INFORMATION: /note= "Exon 8"
; FEATURE:
; NAME/KEY: exon
; LOCATION: 14130..14985
; OTHER INFORMATION: /note= "Exon 9"
; PCT-US96-06231A-6

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Query Match      82.2%; Score 14.8; DB 5; Length 14985;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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```

QY      1  CCGGAAAGCAGCTGCGC 18
DB      10738 CCGGAAAGCAGCTGCC 10721

```

```

RESULT 41
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
US-09-103-840A-2

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```

Query Match      82.2%; Score 14.8; DB 3; Length 4403765;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      1  CCGGAAAGCAGCTGCGC 18
DB      1092940 CCGGACGCGAGCTGCC 1092923

```

```

RESULT 42
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.

```

APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match
Best Local Similarity 82.2%; Score 14.8; DB 3; Length 4411529;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGCTGTCG 18
Db 1092941 CCGGAGGCGAGCTGTCG 1092924

RESULT 43
US-09-621-976-11048/c
Sequence 11048, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 11048
LENGTH: 252
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 148
OTHER INFORMATION: n=a, g, c or t
US-09-621-976-11048

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 4; Length 252;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCGGAGGCGAGCTG 16
Db 107 CCGGAGGCGAGCTG 92

RESULT 44
US-08-256-077-3
Sequence 3, Application US/08256077
Patent No. 5654188
GENERAL INFORMATION:
APPLICANT: Ellmeier, Wilfried
APPLICANT: Weith, Andreas
TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,077
FILING DATE: 23-JUNE-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bismond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1360000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-256-077-3

Query Match
Best Local Similarity 80.0%; Score 14.4; DB 1; Length 360;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CCGAGGCGAGCTGTCG 18
Db 53 CCGAGGCGAGCTGTCG 68

RESULT 45
US-08-466-127-3
Sequence 3, Application US/08466127
Patent No. 5683878
GENERAL INFORMATION:
APPLICANT: Ellmeier, Wilfried
APPLICANT: Weith, Andreas
TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,127
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bismond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1360002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 360 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 1.357
US-08-466-127-3

Query Match
Best Local Similarity 80.0%; Score 14.4; DB 1; Length 360;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGAAGCGAGTCTGGC 18
|||||
Db 53 CGAAGCGAGTCTGGC 68

RESULT 46
US-08-256-077-1
Sequence 1, Application US/08256077
Patent No. 5654188
GENERAL INFORMATION:
APPLICANT: Elimeier, Wilfried
APPLICANT: Weith, Andreas
TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,077
FILING DATE: 23-JUN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1360000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 982 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-256-077-1

Query Match
Best Local Similarity 93.8%; Score 14.4; DB 1; Length 982;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGAAGCGAGTCTGGC 18
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Db 176 CGAAGCGAGTCTGGC 191

RESULT 47
US-08-466-127-1
Sequence 1, Application US/08466127
Patent No. 5683878
GENERAL INFORMATION:
APPLICANT: Elimeier, Wilfried
APPLICANT: Weith, Andreas
TITLE OF INVENTION: Neuroblastoma-Associated Regulator Gene
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Avenue, Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,127
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Esmond, Robert W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 0652.1360002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2540
TELEFAX: (202) 371-2600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 982 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 37...481
US-08-466-127-1

Query Match
Best Local Similarity 80.0%; Score 14.4; DB 1; Length 982;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGAAGCGAGTCTGGC 18
|||||
Db 176 CGAAGCGAGTCTGGC 191

RESULT 48
US-09-566-921-7/c
Sequence 7, Application US/09566921
Patent No. 6682888
GENERAL INFORMATION:
APPLICANT: Loring, Jeanne F.
APPLICANT: Tingley, Debora W.
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
FILE REFERENCE: PA-0024 US
CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL Program
SEQ ID NO 7
LENGTH: 8137
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6682888 411474.10
NAME/KEY: unsure
LOCATION: 3488-3788
OTHER INFORMATION: a, t, c, g, or other
US-09-566-921-7

Query Match
Best Local Similarity 77.8%; Score 14; DB 4; Length 8137;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GGAAGGCACTTG 17
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Db 6246 GGAAGGCACTTG 6233

RESULT 49

US-08-721-986-1/c

; Sequence 1, Application US/08721986

; Patent No. 6103513

; GENERAL INFORMATION:

; APPLICANT: NICHOLSON, DONALD W.

; APPLICANT: ALI, AMBERDEEN

; APPLICANT: VAILLANCOURT, JOHN P.

; APPLICANT: MUNDAY, NEIL A.

; TITLE OF INVENTION: DNA ENCODING PRECURSOR OF

; TITLE OF INVENTION: INTERLEUKIN-1BETA CONVERTING ENZYME -RELATED CYSTEINE

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: JOSEPH A. COPPOLA

; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE

; CITY: RAHWAY

; STATE: NEW JERSEY

; COUNTRY: U.S.A.

; ZIP: 07065

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/721,986

; FILING DATE:

; CLASSIFICATION:

; PRIORITY APPLICATION DATA:

; APPLICATION NUMBER: US/08/225,487

; FILING DATE: 08-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: COPPOLA, JOSEPH A.

; REGISTRATION NUMBER: 38,413

; REFERENCE/DOCKET NUMBER: 19038

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 908-594-6734

; TELEFAX: 908-594-4720

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 157 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-721-986-1

QY 1 CCCGAAAGGCACTTG 17
|||||
Db 103 CCCGAAAGGCACTCG 87

RESULT 50

US-08-225-487A-1/c

; Sequence 1, Application US/08225487A

; Patent No. 6110701

; GENERAL INFORMATION:

; APPLICANT: NICHOLSON, DONALD W.

; APPLICANT: ALI, AMBERDEEN

; APPLICANT: VAILLANCOURT, JOHN P.

; APPLICANT: MUNDAY, NEIL A.

; TITLE OF INVENTION: DNA ENCODING PRECURSOR OF

;; TITLE OF INVENTION: INTERLEUKIN-1BETA CONVERTING ENZYME -RELATED CYSTEINE
;; NUMBER OF SEQUENCES: 9
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: JOSEPH A. COPPOLA
;; STREET: P.O. BOX 2000, 126 E. LINCOLN AVENUE
;; CITY: RAHWAY
;; STATE: NEW JERSEY
;; COUNTRY: U.S.A.
;; ZIP: 07065

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/225,487A

; FILING DATE: 08-APR-1994

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: COPPOLA, JOSEPH A.

; REGISTRATION NUMBER: 38,413

; REFERENCE/DOCKET NUMBER: 19038

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 908-594-6734

; TELEFAX: 908-594-4720

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 157 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; US-08-225-487A-1

Query Match 76.7%; Score 13.8; DB 3; Length 157;
Best Local Similarity 88.2%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCGAAAGGCACTTG 17
|||||
Db 103 CCCGAAAGGCACTCG 87

Search completed: March 5, 2004, 01:18:20
Job time : 98 secs

DEFINITION AGENCOURT 1015199 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6528131
5', mRNA sequence.
ACCESSION BU902747
VERSION BU902747.1 GI:24084660
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Plate: LLM14126 row: c column: 11
High quality sequence stop: 688.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6528131"
/tissue_type="telomysarcoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_71"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.1 kb."
ORIGIN
Query Match 100.0%; Score 18; DB 13; Length 817;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCGAGGAGCAGTCTGCG 18
DB 88 CCCGAGGAGCAGTCTGCG 71
RESULT 48
BO224113 818 bp mRNA linear EST 02-MAY-2002
LOCUS BO224113
DEFINITION AGENCOURT_7558930 NIH_MGC_92 Homo sapiens cDNA clone IMAGE:6045260
5', mRNA sequence.
ACCESSION BO224113
VERSION BO224113.1 GI:20405513
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Plate: LLM13389 row: c column: 21

FEATURES High quality sequence stop: 644.
Location/Qualifiers
1..818
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6045260"
/tissue_type="embryonal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_92"
/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dt primed. Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library."
ORIGIN
Query Match 100.0%; Score 18; DB 13; Length 818;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCGAGGAGCAGTCTGCG 18
DB 112 CCCGAGGAGCAGTCTGCG 95
RESULT 49
BO228424 832 bp mRNA linear EST 02-MAY-2002
LOCUS BO228424/c
DEFINITION AGENCOURT_7657440 NIH_MGC_68 Homo sapiens cDNA clone IMAGE:6059449
5', mRNA sequence.
ACCESSION BO228424
VERSION BO228424.1 GI:20409824
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: DCRD/DTG/Gardar
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
Plate: LLM13326 row: c column: 02
High quality sequence stop: 611.
Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6059449"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_id="NIH_MGC_68"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.8 kb. Library constructed by Life Technologies."
ORIGIN
Query Match 100.0%; Score 18; DB 13; Length 832;
Best Local Similarity 100.0%; Pred. No. 6.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCGAGGAGCAGTCTGCG 18

Db |||||
174 CCCGGAAGCAGCTGGC 157

RESULT 50
AU139600/c

847 bp mRNA linear EST 02-AUG-2002

LOCUS

DEFINITION AU139600 PLACE1 Homo sapiens cDNA clone PLACE1010955 5', mRNA

sequence.

AU139600

ACCESSION

VERSION AU139600.1 GI:11001121

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)

REFERENCE

AUTHORS

Isogai, T.

Yamamoto, U., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and

Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 847)

Isogai, T.

HRI human CDNA project

Unpublished (2000)

CONTACT: Takao Isogai

Genomics Laboratory

Helix Research Institute

1532-3 Yana, Kisarazu, Chiba 292-0812, Japan

Tel: 81-438-52-3975

Fax: 81-438-52-3986

Email: genomics@hri.co.jp

HRI human CDNA project; 5'- & 3'-end one pass sequencing; Helix

Research Institute; cDNA library construction; Department of

Virology, Institute of Medical Science, University of Tokyo, and

Helix Research Institute.

Location/Qualifiers

1..847

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="PLACE1010955"

/tissue_type="Placenta"

/clone_lib="PLACE1"

/note="Vector: pME18SFL3"

ORIGIN

Query Match

Best Local Similarity

Matches

18; Conservative

0; Mismatches

0; Indels

0; Caps

0;

QY

1

CCCGGAAGCAGCTGGC 18

Db

669

CCCGGAAGCAGCTGGC 652

Search completed: March 5, 2004, 01:16:44

Job time : 2545 secs